



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 109804

TO: Sumesh Kaushal
Location: cm1/12a07/11e12
Art Unit: 1636
December 13, 2003

Case Serial Number: 09/205658

From: P. Sheppard
Location: CM1-1E03
Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

* hcpm & hcpm files removed -sk

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:28:11 ; Search time 15.8324 Seconds
(without alignments)
2496.336 Million cell updates/sec

Title: US-09-205-658A-309
Perfect score: 1362
Sequence: 1 I I K I V S R K R Y O E D G F D L R R E D K F N Y F P Q L P V C G D 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1362	100.0	249	21 AAB13325	Caenorhabditis ele
2	1354	99.4	383	19 AAW61534	Homo sapiens P-TEN
3	1354	99.4	394	20 AAY07457	Dog tumour suppress
4	1354	99.4	403	19 AAW64784	Human tumour suppress
5	1354	99.4	403	20 AAY07462	Mouse MMAC1 protei
6	1354	99.4	403	20 AAY07467	Dog MMAC1 protei
7	1354	99.4	403	20 AAY07468	Mouse MMAC1 protei
8	1354	99.4	403	20 AAY07451	Mouse tumour suppress
9	1354	99.4	403	20 AAY07444	Human tumour suppress

10	1354	99.4	403	20	AAW97802	Dual specificity p
11	1354	99.4	403	21	AAW80119	Human PTEN protein
12	1354	99.4	403	22	AAU08939	Human protein phos
13	1354	99.4	403	22	AAG67452	Amino acid sequenc
14	1354	99.4	403	22	AAG67631	Amino acid sequenc
15	1354	99.4	403	23	ABP65106	Hypoxia-induced pr
16	1354	99.4	403	23	AAE24851	Human phosphoinosi
17	1354	99.4	403	23	AAE17879	Human PTEN protein
18	1354	99.4	430	20	AAV07458	Dog TS10q23.3 gene
19	1354	99.4	559	20	AAV07456	Mouse TS10q23.3 ge
20	1354	99.4	565	18	AAW34402	Protein encoded by
21	1354	99.4	597	20	AAW07450	Human TS10q23.3 ge
22	1348	99.0	403	19	AAW64786	Human tumour suppress
23	1348	99.0	403	23	AAE17900	Human PTEN protein
24	1346	98.8	403	19	AAW64785	Human tumour suppress
25	1346	98.8	403	23	AAE17898	Human PTEN protein
26	1346	98.8	403	23	AAE17899	Human PTEN protein
27	1344	98.7	403	23	AAE17897	Human PTEN protein
28	641.5	47.1	509	22	ABB61711	Drosophila melanog
29	641.5	47.1	509	22	ABB66720	Drosophila melanog
30	641.5	47.1	514	22	ABB66721	Drosophila melanog
31	507	37.2	550	24	AAE32030	Human kinase and p
32	478	35.1	551	22	AAG67459	Amino acid sequenc
33	478	35.1	551	22	AAG67638	Amino acid sequenc
34	465	34.1	962	21	AAE13326	Caenorhabditis ele
35	453	33.3	248	21	AAE13324	Human PTEN phospho
36	453	33.3	477	24	ABU07383	Human protein NOV1
37	439	32.2	85	22	ABG51931	Human liver peptid
38	439	32.2	85	22	ABG31862	Peptide #4513 enco
39	439	32.2	85	22	ABB37098	Peptide #4604 enco
40	439	32.2	85	22	ABB22407	Protein #4406 enco
41	439	32.2	85	22	AAW57820	Human brain expres
42	439	32.2	85	22	AAW70234	Human bone marrow
43	439	32.2	85	22	AAW18060	Peptide #4494 enco
44	439	32.2	85	22	AAW30572	Peptide #4609 enco
45	439	32.2	85	22	AAW05700	Peptide #4382 enco

ALIGNMENTS

RESULT 1

AAB13325
ID AAB13325 standard; Protein; 249 AA.

AC AAB13325;

XX AAB13325;

DT 12-JAN-2001 (first entry)

XX Caenorhabditis elegans DAF-18 phosphatase domain.

DE Caenorhabditis elegans; daf-18; insulin signalling pathway;

KW daf-2; ags-1; insulin receptor; PI-3-kinase; PKB kinase;

KW PTEN lipid phosphatase; antidiabetic; anorectic; diabetes.

XX Caenorhabditis elegans.

OS WO200033068-A1.

PN 08-JUN-2000.

PD 02-DEC-1999; 99WO-US28529.

PF 03-DEC-1998; 98US-0205658.

XX (GSHO) GEN HOSPITAL CORP.

XX Ruvkun G, Ogg S;

XX WPI; 2000-423022/36.

XX Diagnosing and treating obesity and impaired glucose tolerance using

PT modulators of daf-18 expression and/or activity -

XX Disclosure; Fig 398; 402pp; English.

XX The present sequence is the phosphatase domain of *Caenorhabditis elegans*

CC DAF-18 protein, which is one of a number of *C. elegans* proteins that have

CC been identified as homologues of proteins in the mammalian insulin

CC signalling pathway. The *C. elegans* age-1 gene encodes a homologue of

CC the mammalian PI 3-kinase whilst *daf-2* encodes a homologue of the

CC mammalian insulin receptor. The *C. elegans* AKT kinase and PKB kinase

CC act downstream of *daf-2* and *age-1*, just as their mammalian homologues

CC act downstream of insulin signalling. The *C. elegans* PTEN lipid

CC phosphatase homologue, DAF-18, has been found to act upstream of AKT in

CC the pathway. This discovery has enabled mammalian PTEN action to be

CC mapped to the insulin signalling pathway. Conserved DAF motifs can be

CC used to design probes to identify mammalian DAF homologues and thus to

CC identify individuals with a predisposition toward the development of

CC glucose intolerance conditions, such as obesity and diabetes.

XX

SQ Sequence 249 AA;

Query Match 100.0%; Score 1362; DB 21; Length 249;

Best Local Similarity 100.0%; Pred. No. 7.6e-147;

Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 60

DB 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 60

QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A A I H 120

DB 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A A I H 120

QY 121 C K A G K R T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180

DB 121 C K A G K R T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 240

DB 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 240

QY 241 P Q L P V C G D 249

DB 241 P Q L P V C G D 249

RESULT 2

AAW61534

ID AAW61534 standard; Protein; 383 AA.

AC AAW61534;

XX

DT 09-NOV-1998 (first entry)

DE Homo sapiens P-TEN tumour suppressor.

XX

KW P-TEN; tumour suppressor; cancer; diagnosis; treatment; glioblastoma;

KW Cowden disease; melanoma; prostate; breast; brain.

XX

OS Homo sapiens.

XX

PN W09834624-A1.

XX

PD 13-AUG-1998.

XX

PF 06-FEB-1998; 98WO-US02615.

XX

PR 07-FEB-1997; 97US-0036943.

XX

PA (COLD-) COLD SPRING HARBOR LAB.

PA (UYCO) UNIV COLUMBIA NEW YORK.

XX

PI Parsons RE, Wigler MH;

XX

DR WPI: 1998-446939/38.

DR N-PSDB; AAV45137.

XX

PT P-TEN tumour suppressor protein and DNA, for treating cancer - and

PT P-TENS with altered, truncated or deleted phosphatase domains, for

PT diagnosing and treating cancer and Cowden disease

XX

PS Claim 9; Fig 4A; 77pp; English.

XX

CC The sequence is that of the P-TEN tumour suppressor protein.

CC It can be used to diagnose cancer (glioblastoma, Cowden disease,

CC melanoma, or cancer of the prostate, breast or brain) by detecting

CC altered P-TEN sequences. Altered protein is detected based on a

CC loss of heterozygosity or a homozygous deletion at the P-TEN locus.

CC Cancer in a patient with altered P-TEN, with reduced or no phosphatase

CC activity, may be treated by introducing into the patient the wild-type

CC sequence. The protein is used to identify compounds which may be useful

CC as drugs for treating cancer, by testing the effects of P-TEN activity

CC on the compounds, or by testing the effect of the compounds on

CC expression of the gene. Such effects are inhibition, activation or

CC enhancement of enzymatic activity, preferably phosphatase activity.

XX

SQ Sequence 383 AA;

Query Match 99.4%; Score 1354; DB 19; Length 383;

Best Local Similarity 99.6%; Pred. No. 1.2e-145;

Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 60

DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A A I H 120

DB 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180

DB 124 C K A G K R T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 240

DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 243

QY 241 P Q L P V C G D 249

DB 244 P Q L P V C G D 252

RESULT 3

AAV07457

ID AAV07457 standard; Protein; 394 AA.

XX

AC AAV07457;

XX

DT 16-JUL-1999 (first entry)

DE Dog tumour suppressor protein TS10q23.3.

XX

KW Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;

KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;

KW enzyme linked immunosorbant assay; gene expression; dog.

XX

OS Canis familiaris.

XX

PN W09910537-A1.

XX

PD 04-MAR-1999.

XX

PF 26-AUG-1998; 98WO-US17636.

XX

PR 30-APR-1998; 98US-0083563.

PR 26-AUG-1997; 97US-0057750.

XX (MYRI-) MYRIAD GENETICS INC.
PA (TEXA) UNIV TEXAS SYSTEM.
XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
PI Yung WKA;
XX WPI; 1999-190638/16.
DR N-PSDB; AAX57673.
XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
PT Syndrome and susceptibility to breast cancer
XX Disclosure; Fig 9; 244pp; English.
XX The invention relates to mutant genes encoding the tumour suppressor
CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
CC gland and endometrium (claimed). The mutant gene is also useful for
CC diagnosing a subject who has a predisposition to breast cancer. Both
CC methods involve antibodies, which specifically bind to a TS10q23.3,
CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
XX Sequence 394 AA;
SQ
Query Match 99.4%; Score 1354; DB 20; Length 394;
Best Local Similarity 99.6%; Pred. No. 1.2e-145;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V V R F L D S K H K N 60
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V I Y S S N S G P T R E D K F N Y F E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V I Y S S N S G P T R E D K F N Y F E F 243
QY 241 P Q L P V C G D 249
DB 244 P Q L P V C G D 252
RESULT 4
AAW64784
ID AAW64784 standard; Protein; 403 AA.
XX AAW64784;
AC AAW64784;
XX 03-NOV-1998 (first entry)
DT Human tumour suppressor TS10q23.3 protein.
DE
XX Tumour suppressor; TS10q23.3; human; diagnosis; tumour; prostate; breast;
KW brain; glioma; metastasis; gene therapy; anti-cancer; transgenic animal;
XX drug screening.
XX Homo sapiens.
OS
XX WO9833907-A1.
PN
XX 06-AUG-1998.
PD
XX 08-JAN-1998; 98WO-US00353.
PF
XX

PR 30-JAN-1997; 97US-0791115.
XX (MYRI-) MYRIAD GENETICS INC.
PA (TEXA) UNIV TEXAS SYSTEM.
XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
PI Yung WKA;
XX WPI; 1998-437461/37.
DR N-PSDB; AAV46392..
XX Tumour suppressor TS10q23.3 and related antibodies - useful for
PT diagnosis, staging and treatment of cancer, especially of breast,
PT prostate and brain
XX Claim 1; Fig 7; 161pp; English.
XX This sequence represents the human tumour suppressor protein TS10q23.3.
CC This protein can be used to diagnose a wide range of tumours,
CC particularly of prostate, breast and brain (glioma), to stage cancers
CC (particularly differentiation between low grade brain cancer and glioma)
CC and for prediction of metastasis. This suppressor and its nucleic acid
CC are also used to alter the phenotype to specifically treat cancer cells,
CC e.g. by in vivo or ex vivo gene therapy, optionally together with other
CC anti-cancer agents. Fragments of the suppressor can be coupled to an
CC immunogenic carrier and are used to raise antibodies, to isolate
CC antigens, as immunoassay reagents, to clone related DNA or for
CC immunotherapy. Antisense nucleic acid can be used to produce transgenic
CC animals (useful for drug screening) or to eliminate dominant negative
CC mutants.
XX Sequence 403 AA;
SQ
Query Match 99.4%; Score 1354; DB 19; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.2e-145;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V V R F L D S K H K N 60
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V I Y S S N S G P T R E D K F N Y F E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V I Y S S N S G P T R E D K F N Y F E F 243
QY 241 P Q L P V C G D 249
DB 244 P Q L P V C G D 252
RESULT 5
AAV07462
ID AAV07462 standard; peptide; 403 AA.
XX AAV07462;
AC AAV07462;
XX 16-JUL-1999 (first entry)
DT Mouse MMAC1 protein sequence.
DE
XX Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
KW enzyme linked immunosorbant assay; gene expression; mouse.
XX Mus musculus.
OS

XX WO9910537-AL.
 PN 04-MAR-1999.
 XX 26-AUG-1998; 98WO-US17636.
 XX 30-APR-1998; 98US-0083563.
 PR 26-AUG-1997; 97US-0057750.
 XX (MYRI-) MYRIAD GENETICS INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
 PI Yung WKA;
 PI WPI; 1999-190638/16.
 XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
 PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
 PT Syndrome and susceptibility to breast cancer
 XX Disclosure; Page.226-227; 244pp; English.
 XX The invention relates to mutant genes encoding the tumour suppressor
 CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
 CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
 CC gland and endometrium (claimed). The mutant gene is also useful for
 CC diagnosing a subject who has a predisposition to breast cancer. Both
 CC methods involve antibodies, which specifically bind to a TS10q23.3.
 CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
 XX Sequence 403 AA;
 SQ
 Query Match 99.4%; Score 1354; DB 20; Length 403;
 Best Local Similarity 99.6%; Pred. No. 1.2e-145;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 60
 Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 63
 QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P O L E I K P F C E D L D Q W L S E D D N H V A A I H 120
 Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P O L E I K P F C E D L D Q W L S E D D N H V A A I H 123
 QY 121 C K A G K G R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
 Db 124 C K A G K G R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183
 QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 240
 Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 243
 QY 241 P Q P L P V C G D 249
 Db 244 P Q P L P V C G D 252
 RESULT 6
 AAY07467
 ID AAY07467 standard; Protein; 403 AA.
 XX AAY07467;
 XX 16-JUL-1999 (first entry)
 DT Dog MMAC1 protein.
 DE Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
 KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
 KW enzyme linked immunosorbant assay; gene expression; dog.
 XX

OS Canis familiaris.
 XX WO9910537-AL.
 PN 04-MAR-1999.
 XX 26-AUG-1998; 98WO-US17636.
 XX 30-APR-1998; 98US-0083563.
 PR 26-AUG-1997; 97US-0057750.
 XX (MYRI-) MYRIAD GENETICS INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
 PI Yung WKA;
 PI WPI; 1999-190638/16.
 XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
 PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
 PT Syndrome and susceptibility to breast cancer
 XX Claim 3; Page 232-233; 244pp; English.
 XX The invention relates to mutant genes encoding the tumour suppressor
 CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
 CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
 CC gland and endometrium (claimed). The mutant gene is also useful for
 CC diagnosing a subject who has a predisposition to breast cancer. Both
 CC methods involve antibodies, which specifically bind to a TS10q23.3.
 CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
 XX Sequence 403 AA;
 SQ
 Query Match 99.4%; Score 1354; DB 20; Length 403;
 Best Local Similarity 99.6%; Pred. No. 1.2e-145;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 60
 Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 63
 QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P O L E I K P F C E D L D Q W L S E D D N H V A A I H 120
 Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P O L E I K P F C E D L D Q W L S E D D N H V A A I H 123
 QY 121 C K A G K G R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180
 Db 124 C K A G K G R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183
 QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 240
 Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F 243
 QY 241 P Q P L P V C G D 249
 Db 244 P Q P L P V C G D 252
 RESULT 7
 AAY07468
 ID AAY07468 standard; Protein; 403 AA.
 XX AAY07468;
 XX 16-JUL-1999 (first entry)
 DT Mouse MMAC1 protein.
 DE Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
 KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
 KW

KW enzyme linked immunosorbant assay; gene expression; mouse.

XX Mus musculus.

XX WO9910537-A1.

XX 04-MAR-1999.

XX 26-AUG-1998; 98WO-US17636.

XX 30-APR-1998; 98US-0083563.

XX 26-AUG-1997; 97US-0057750.

XX (MYRI-) MYRIAD GENETICS INC.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;

XX Yung WKA;

XX WPI; 1999-190638/16.

XX N-PSDB; AAX57700.

XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour

XX suppressor (TS10q23.3) - useful for the diagnosis of Cowden's

XX Syndrome and susceptibility to breast cancer

XX PT Disclosure; Page 236-238; 244pp; English.

XX PS The invention relates to mutant genes encoding the tumour suppressor

XX TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of

XX Cowden's Syndrome in cells selected from the breast, ovaries, thyroid

XX gland and endometrium (claimed). The mutant gene is also useful for

XX diagnosing a subject who has a predisposition to breast cancer. Both

XX methods involve antibodies, which specifically bind to a TS10q23.3,

XX used in an ELISA assay to evaluate the level of TS10q23.3 expression.

XX SQ Sequence 403 AA;

XX Query Match 99.4%; Score 1354; DB 20; Length 403;

XX Best Local Similarity 99.6%; Pred. No. 1.2e-145;

XX Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 1 I I K E I V S N K R R Y Q D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V V R F L D S K H N 60

XX 4 I I K E I V S N K R R Y Q D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V V R F L D S K H N 63

XX 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A A I H 120

XX 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A A I H 123

XX 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180

XX 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183

XX 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V I Y S N S G P T R E D K F N Y P E F 240

XX 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V I Y S N S G P T R E D K F N Y P E F 243

XX 241 P Q P L P V C G D 249

XX 244 P Q P L P V C G D 252

XX RESULT 8

XX AAY07451

XX ID AAY07451 standard; Protein; 403 AA.

XX AC AAY07451;

XX 16-JUL-1999 (first entry)

XX Mouse tumour suppressor protein TS10q23.3.

KW Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
XX enzyme linked immunosorbant assay; gene expression; mouse.

XX Mus musculus.

XX WO9910537-A1.

XX 04-MAR-1999.

XX 26-AUG-1998; 98WO-US17636.

XX 30-APR-1998; 98US-0083563.

XX 26-AUG-1997; 97US-0057750.

XX (MYRI-) MYRIAD GENETICS INC.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;

XX Yung WKA;

XX WPI; 1999-190638/16.

XX N-PSDB; AAX57672.

XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour

XX suppressor (TS10q23.3) - useful for the diagnosis of Cowden's

XX Syndrome and susceptibility to breast cancer

XX PS Disclosure; Fig 9; 244pp; English.

XX CC The invention relates to mutant genes encoding the tumour suppressor

XX TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of

XX Cowden's Syndrome in cells selected from the breast, ovaries, thyroid

XX gland and endometrium (claimed). The mutant gene is also useful for

XX diagnosing a subject who has a predisposition to breast cancer. Both

XX methods involve antibodies, which specifically bind to a TS10q23.3,

XX used in an ELISA assay to evaluate the level of TS10q23.3 expression.

XX SQ Sequence 403 AA;

XX Query Match 99.4%; Score 1354; DB 20; Length 403;

XX Best Local Similarity 99.6%; Pred. No. 1.2e-145;

XX Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 1 I I K E I V S N K R R Y Q D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V V R F L D S K H N 60

XX 4 I I K E I V S N K R R Y Q D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V V R F L D S K H N 63

XX 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A A I H 120

XX 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A A I H 123

XX 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 180

XX 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183

XX 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V I Y S N S G P T R E D K F N Y P E F 240

XX 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V I Y S N S G P T R E D K F N Y P E F 243

XX 241 P Q P L P V C G D 249

XX 244 P Q P L P V C G D 252

XX RESULT 9

XX AAY07444

XX ID AAY07444 standard; Protein; 403 AA.

XX AC AAY07444;

XX 16-JUL-1999 (first entry)

DE Human tumour suppressor protein TS10q23.3.
 XX Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
 KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
 KW enzyme linked immunosorbant assay; gene expression; human.
 OS Homo sapiens.
 XX WO9910537-A1.
 PN 04-MAR-1999.
 XX 26-AUG-1998; 98WO-US17636.
 XX 30-APR-1998; 98US-0083563.
 PR 26-AUG-1997; 97US-0057750.
 XX (MYRI-) MYRIAD GENETICS INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
 PI Yung WKA;
 XX WPI; 1999-190638/16.
 DR N-PSDB; AAX57671.
 XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
 PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
 PT Syndrome and susceptibility to breast cancer
 XX Disclosure; Fig 7; 244pp; English.
 XX The invention relates to mutant genes encoding the tumour suppressor
 CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
 CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
 CC gland and endometrium (claimed). The mutant gene is also useful for
 CC diagnosing a subject who has a predisposition to breast cancer. Both
 CC methods involve antibodies, which specifically bind to a TS10q23.3,
 CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
 XX Sequence 403 AA;
 SQ
 Query Match 99.4%; Score 1354; DB 20; Length 403;
 Best Local Similarity 99.6%; Pred. No. 1.2e-145;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V R F L D S K H K N 60
 Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V R F L D S K H K N 63
 QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A I H 120
 Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A I H 123
 QY 121 C K A G K R G T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V T R D K G V T I P S O R R Y V Y Y S Y L L K 180
 Db 124 C K A G K R G T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V T R D K G V T I P S O R R Y V Y Y S Y L L K 183
 QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V W C Q L K V I Y S S N S G P T R R E D K F N Y F E F 240
 Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V W C Q L K V I Y S S N S G P T R R E D K F N Y F E F 243
 QY 241 P Q P L P V C G D 249
 Db 244 P Q P L P V C G D 252
 RESULT 10
 AAW97802
 ID AAW97802 standard; Protein; 403 AA.
 XX
 AC AAW97802;
 XX

DT 21-MAY-1999 (first entry)
 XX Dual specificity phosphatase PTEN.
 DE PTEN; MMAC1; protein tyrosine phosphatase; human; prostate cancer;
 XX brain cancer; prostate cancer; tumour suppressor; Cowden's disease;
 KW neurodegenerative disease; Parkinson's disease; diagnosis; therapy.
 KW Homo sapiens.
 OS WO9902704-A2.
 PN 21-JAN-1999.
 XX 08-JUL-1998; 98WO-US14205.
 XX 29-JUN-1998; 98US-0090984.
 PR 08-JUL-1997; 97US-0051908.
 XX (COLD-) COLD SPRING HARBOR LAB.
 PA Myers MP, Tonks NK;
 XX WPI; 1999-120905/10.
 DR N-PSDB; AAX07339.
 XX New use of PTEN phosphatase - for developing products for the
 PT diagnosis and treatment of hyperproliferative disorders, e.g.
 PT cancers or neurodegenerative disorders such as Parkinson's disease
 XX Disclosure; Fig 1A-C; 60pp; English.
 XX This is the amino acid sequence of human PTEN phosphatase,
 CC predicted from the PTEN gene (see AAX07339) located at 10q22-23.
 CC PTEN shares homology with the protein tyrosine phosphatase
 CC family. It can function as a dual specificity phosphatase in
 CC viro, displaying selectivity for extremely acidic substrates.
 CC PTEN dephosphorylates phosphatidylinositol in vitro, and displays
 CC selectivity for the 3 position of the inositol ring. It is also
 CC able to dephosphorylate serine, threonine and tyrosine residues
 CC when present in acidic substrates. The phosphatase activity of
 CC PTEN is required for its ability to function as a tumour suppressor
 CC or an apoptosis inducer. Point mutations, including point mutations
 CC in tumour samples and Cowden's disease kindreds, ablate PTEN
 CC activity. PTEN functions as an upstream, negative regulator of
 CC PKB/Akt and has the potential to regulate signals associated with
 CC control of cell survival. PTEN polypeptides and polynucleotides
 CC can be used in the diagnosis and treatment of conditions
 CC characterised by an alteration in PTEN which causes an alteration
 CC of phosphatase activity. They can be used to treat
 CC hyperproliferative conditions such as cancers, e.g. brain, prostate
 CC or breast cancers or Cowden's disease, or other hyperproliferative
 CC diseases involving reduced phosphatase activity. They can also be
 CC used in methods of reducing PTEN phosphatase activity for treating
 CC conditions such as Parkinson's disease and other neurodegenerative
 CC disease.
 XX Sequence 403 AA;
 SQ
 Query Match 99.4%; Score 1354; DB 20; Length 403;
 Best Local Similarity 99.6%; Pred. No. 1.2e-145;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V R F L D S K H K N 60
 Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y R N N I D D V R F L D S K H K N 63
 QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A I H 120
 Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A I H 123
 QY 121 C K A G K R G T G V M I C A V L L H R G K F L K A Q E A L D F Y G E V T R D K G V T I P S O R R Y V Y Y S Y L L K 180
 XX

Db 124 CKAGKGTGVMICAYLLHRGKFLKAQALDFYGEVTRDKKGVTPISQRRVYVYVYLLK 183
Qy 181 NHDYRPVALLFHQMFTIPMFSGGTCNPFVVCQKVKIYSSNSGPTREDKFNYPF 240
Db 184 NHDYRPVALLFHQMFTIPMFSGGTCNPFVVCQKVKIYSSNSGPTREDKFNYPF 243
Qy 241 POPLPVCGD 249
Db 244 POPLPVCGD 252

RESULT 11
AAU80119
ID AAU80119 standard; Protein; 403 AA.
XX
AC AAU80119;
DT 22-MAY-2000 (first entry)
XX
DE Human PTEN protein sequence SEQ ID NO:1.
XX
KW Human; PTEN; MMAC1; TEPI; phosphothioate; antisense oligonucleotide;
KW inhibition; protein phosphatase; tumour; diagnosis; inflammation;
KW anticancer; anti-inflammatory; anti-infective; infection.
XX
OS Homo sapiens.
XX
FN US6020199-A.
XX
PD 01-FEB-2000.
XX
PF 21-JUL-1999; 99US-0358381.
XX
PR 21-JUL-1999; 99US-0358381.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowsert LM;
XX
DR WPI; 2000-181363/16.
XX
DR N-PSDB; AAZ91361.
XX
XX
PT New antisense compounds useful for treating, preventing or diagnosing
PT e.g. tumors or inflammation, are targeted to the human dual specificity
PT protein phosphatase (PTEN) sequence
XX
PS Claim 1; Column 43-46; 32pp; English.
XX
CC The present invention describes phosphorothioate antisense
CC oligonucleotides that are targeted to the 3'-untranslated region (UTR)
CC of the sequence encoding a human dual specificity protein phosphatase
CC designated PTEN (also known as MMAC1 and TEPI), and hybridise
CC specifically to the human PTEN nucleotide sequence given in AAZ91361.
CC The antisense oligonucleotides have anticancer, anti-inflammatory and
CC anti-infective activities. The phosphorothioate antisense
CC oligonucleotides can be used for diagnosis, treatment and prevention of
CC PTEN-related diseases, e.g. infections, inflammation and tumours.
CC The present sequence represents the human PTEN protein sequence.
XX
SQ Sequence 403 AA;

Query Match 99.4%; Score 1354; DB 21; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.2e-145;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S R N K R Y Q E D G F D L D T Y P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H N 60
Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H N 63
Qy 61 H Y K I N L C A E R H Y D T A K E N C R V A Q P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A I H 120
Db 64 H Y K I N L C A E R H Y D T A K E N C R V A Q P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A I H 123

Qy 121 CKAGKGTGVMICAYLLHRGKFLKAQALDFYGEVTRDKKGVTPISQRRVYVYVYLLK 180
Db 124 CKAGKGTGVMICAYLLHRGKFLKAQALDFYGEVTRDKKGVTPISQRRVYVYVYLLK 183
Qy 181 NHDYRPVALLFHQMFTIPMFSGGTCNPFVVCQKVKIYSSNSGPTREDKFNYPF 240
Db 184 NHDYRPVALLFHQMFTIPMFSGGTCNPFVVCQKVKIYSSNSGPTREDKFNYPF 243
Qy 241 POPLPVCGD 249
Db 244 POPLPVCGD 252

RESULT 12
AAU08939
ID AAU08939 standard; Protein; 403 AA.
XX
AC AAU08939;
DT 18-DEC-2001 (first entry)
XX
DE Human protein phosphatase PTEN.
XX
KW Human; PTEN; MMAC1; TEPI; protein phosphatase; antisense;
KW antiinflammatory; cytostatic; antidiabetic; antilipaeamic;
KW infection; inflammation; tumour; diabetes; insulin resistance;
KW insulin sensitivity; triglyceride control; cholesterol control.
XX
OS Homo sapiens.
XX
FN US6284538-B1.
XX
PD 04-SEP-2001.
XX
PF 24-MAY-2000; 2000US-0577902.
XX
PR 21-JUL-1999; 99US-0358381.
XX
PR 14-DEC-1999; 99WO-US29594.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowsert LM, McKay R;
XX
DR WPI; 2001-588976/66.
XX
DR N-PSDB; AAS13987.
XX
PT New antisense oligonucleotides targeting nucleic acids encoding PTEN,
PT useful for treating diabetes, increasing insulin sensitivity, or
PT decreasing insulin resistance, blood triglyceride or cholesterol levels
PT in a diabetic animal
XX
PS Example 13; Column 53-55; 38pp; English.
XX
CC The invention relates to a compound targeted to a nucleic acid encoding
CC PTEN (a dual specificity protein phosphatase), where the compound is an
CC antisense oligonucleotide. The antisense oligonucleotides are useful in
CC modulating the function of nucleic acids encoding PTEN, ultimately
CC modulating the amount of PTEN produced. The antisense compounds can be used
CC as diagnostics, therapeutics, prophylactics (e.g. to prevent or delay
CC infection, inflammation or tumour formation), and as research agents and
CC kits. The antisense compounds are also useful in treating diabetes,
CC decreasing insulin resistance, increasing insulin sensitivity and
CC decreasing blood triglyceride or cholesterol levels in a diabetic animal.
CC The present sequence is human PTEN (also known as MMAC1/TEPI).
XX
SQ Sequence 403 AA;

Query Match 99.4%; Score 1354; DB 22; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.2e-145;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S R N K R Y Q E D G F D L D T Y P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H N 60
Db 1 I I K E I V S R N K R Y Q E D G F D L D T Y P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H N 60

Db 4 I I K E I V S R N K R Y Q E D G F D L D T I Y P N I I A M F P A E R L E G V Y R N N I D D V R F L D S K H K N 63
 QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
 Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
 QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
 Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183
 QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y P E F 240
 Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y P E F 243
 QY 241 P O P L P V C G D 249
 Db 244 P O P L P V C G D 252

RESULT 13
 AAG67452
 ID AAG67452 standard; Protein; 403 AA.
 AC AAG67452;
 DT 26-NOV-2001 (first entry)
 XX Amino acid sequence of a human polypeptide.
 DE Human; protein kinase; protein phosphatase; signal transduction;
 KW intracellular signalling pathway.
 KW Homo sapiens.
 OS
 XX
 PN WO200109345-A1.
 XX
 PD 08-FEB-2001.
 XX
 PF 28-JUL-2000; 2000WO-JP05060.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 18-OCT-1999; 99US-0159590.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 17-FEB-2000; 2000US-0183322.
 PR 02-MAY-2000; 2000JP-0183767.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 PI Senoo C, Nezu J;
 XX
 DR WPI; 2001-564736/63.
 XX
 XX New genes encoding protein kinase and protein phosphatase, useful for
 PT identifying modulators which can be used to treat human or animal
 PT disorders associated with the expression or function of these enzymes -
 XX
 PS Example 4; Page 288-291; 336pp; Japanese.
 XX
 XX The specification describes human protein kinase/protein phosphatases.
 CC The polypeptides are expected to participate in signal transduction
 CC in cells. The kinase phosphatases are connected with intracellular
 CC signalling pathways. Antisense oligonucleotides and compounds
 CC identified by screening (agonists or antagonists) can be used to
 CC treat human or animal disorders associated with the expression
 CC or function of the protein. In addition, the polypeptides may be used
 CC as target molecules for drug development. The present sequence
 CC represents a polypeptide, used in the course of the invention.
 XX
 SQ Sequence 403 AA;
 Query Match 99.4%; Score 1354; DB 22; Length 403;

Best Local Similarity 99.6%; Pred. No. 1.2e-145;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 I I K E I V S R N K R Y Q E D G F D L D T I Y P N I I A M F P A E R L E G V Y R N N I D D V R F L D S K H K N 60
 Db 4 I I K E I V S R N K R Y Q E D G F D L D T I Y P N I I A M F P A E R L E G V Y R N N I D D V R F L D S K H K N 63
 QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
 Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
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 Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183
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 QY 241 P O P L P V C G D 249
 Db 244 P O P L P V C G D 252
 RESULT 14
 AAG67631
 ID AAG67631 standard; Protein; 403 AA.
 AC AAG67631;
 DT 26-NOV-2001 (first entry)
 XX Amino acid sequence of a human protein.
 DE Human; protein kinase; protein phosphatase; signal transduction.
 KW Homo sapiens.
 OS
 XX
 PN WO200109316-A1.
 XX
 PD 08-FEB-2001.
 XX
 PF 28-JUL-2000; 2000WO-JP05061.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 18-OCT-1999; 99US-0159590.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 17-FEB-2000; 2000US-0183322.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 PI Senoo C, Nezu J;
 XX
 DR WPI; 2001-570286/64.
 XX
 XX New genes encoding proteins with protein kinase/protein phosphatase
 PT activity, useful in the diagnosis and treatment of diseases -
 XX
 PS Example 4; Page 188-191; 233pp; Japanese.
 CC The specification describes human protein kinase/protein phosphatases.
 CC It is expected that the protein kinase/protein phosphatase gene
 CC participates in signal transduction in cells. The protein
 CC kinase/protein phosphatase polypeptides and polynucleotides are
 CC useful for developing diagnostics and treatment agents for human
 CC and animal diseases. The protein kinase/protein phosphatase polypeptides
 CC are useful as target molecules in designing novel drugs. The protein
 CC kinase/protein phosphatase polynucleotides are useful as a source of
 CC probes and primers, which may be used to isolate homologous sequences.

The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV7873-ABV78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumorigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, presclapmsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythroplasia or hair loss.

1	IIKEIVSRNKRRYQBDGFDLDTIYYPNTIANGFPAERLEGVYVRNNDVVRFDSKHKH	60
4	IIKEIVSRNKRRYQBDGFDLDTIYYPNTIANGFPAERLEGVYVRNNDVVRFDSKHKH	63
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121	CKAGKGRGTGVMICAYLLHRGKFLKAQEALDFGEVTRDRKKGVTIIPQSRRYVYVYSLK	180
124	CKAGKGRGTGVMICAYLLHRGKFLKAQEALDFGEVTRDRKKGVTIIPQSRRYVYVYSLK	183
181	NHLDYRPVALLPHKMMFETIPMFSGTGCNPFQVVCOLKVKIYSSNSGPTTRREDKFNFEF	240
184	NHLDYRPVALLPHKMMFETIPMFSGTGCNPFQVVCOLKVKIYSSNSGPTTRREDKFNFEF	243
241	POPLPVCGD	249
244	POPLPVCGD	252

Search completed: December 10, 2003, 20:32:15
Job time : 16.8324 secs

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QY      181 NHLDYRPPVALLFHKMMFETIPMFSGGTCNPOQFVVCOLKVKIYSSNSGPTRRDKFMYFEF 240
Db      184 NHLDYRPPVALLFHKMMFETIPMFSGGTCNPOQFVVCOLKVKIYSSNSGPTRRDKFMYFEF 243
QY      241 POPLPVCGD 249
Db      244 POPLPVCGD 252

Search completed: December 10, 2003, 20:32:15
Job time : 16.8324 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:30:47 ; Search time 6.16846 Seconds
(without alignments)
1707.948 Million cell updates/sec

Title: US-09-205-658A-309

Perfect score: 1362

Sequence: 1 IIKIVSRNKRKYQEDGFDL.....RRDKFNFFPQLPVCGD 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42110858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1354	99.4	394	3	US-08-791-115B-27
2	1354	99.4	394	4	US-09-140-749-17
3	1354	99.4	403	3	US-08-791-115B-1
4	1354	99.4	403	3	US-08-791-115B-23
5	1354	99.4	403	3	US-08-791-115B-25
6	1354	99.4	403	4	US-09-140-749-2
7	1354	99.4	403	4	US-09-140-749-10
8	1354	99.4	403	4	US-09-140-749-49
9	1354	99.4	403	4	US-09-140-749-55
10	1354	99.4	403	4	US-09-140-749-57
11	1354	99.4	430	3	US-08-791-115B-7
12	1354	99.4	430	4	US-09-140-749-18
13	1354	99.4	559	4	US-09-140-749-15
14	1354	99.4	565	3	US-08-906-156A-12
15	1354	99.4	597	4	US-09-140-749-8
16	1354	99.4	645	3	US-08-791-115B-5
17	1354	99.4	742	3	US-08-791-115B-5
18	294	21.6	60	3	US-08-791-115B-20
19	294	21.6	60	4	US-09-140-749-31
20	287	21.1	60	3	US-08-791-115B-19
21	287	21.1	60	4	US-09-140-749-30
22	286	21.0	60	3	US-08-791-115B-21
23	286	21.0	60	4	US-09-140-749-32
24	121.5	8.9	170	3	US-08-725-532A-1
25	121.5	8.9	173	3	US-08-725-532A-6
26	121.5	8.9	173	3	US-09-164-193-20
27	121.5	8.9	173	4	US-09-221-448A-20

28 120 8.8 278 3 US-08-821-278A-18 Sequence 18, Appl
29 120 8.8 802 3 US-09-081-345-18 Sequence 18, Appl
30 113 8.3 594 4 US-09-468-872-2 Sequence 2, Appl
31 112.5 8.3 167 3 US-08-725-532A-5 Sequence 5, Appl
32 109 8.0 173 3 US-08-725-532A-3 Sequence 3, Appl
33 109 8.0 173 3 US-09-164-193-2 Sequence 2, Appl
34 109 8.0 173 4 US-08-221-448A-2 Sequence 2, Appl
35 107 7.9 22 3 US-08-906-156A-76 Sequence 76, Appl
36 102.5 7.5 807 3 US-09-081-345-2 Sequence 2, Appl
37 102 7.5 289 1 US-08-036-210-13 Sequence 13, Appl
38 102 7.5 289 2 US-08-449-609-13 Sequence 13, Appl
39 102 7.5 289 4 US-09-361-096A-13 Sequence 7, Appl
40 101 7.4 250 2 US-08-685-932-7 Sequence 7, Appl
41 101 7.4 250 2 US-09-144-925-7 Sequence 22, Appl
42 99 7.3 277 2 US-08-685-932-22 Sequence 22, Appl
43 99 7.3 277 1 US-09-144-925-22 Sequence 22, Appl
44 98.5 7.2 116 1 US-07-988-273-5 Sequence 5, Appl
45 98.5 7.2 116 5 PCT-US93-12019-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-08-791-115B-27
; Sequence 27, Application US/08791115B
; Patent No. 6262242
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, W.K. Alfred
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08791.115B
; FILING DATE: 30-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 38,957
; REFERENCE/DOCKET NUMBER: 2318-134.A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-683-6040
; TELEFAX: 202-683-7031
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-115B-27

Query Match 99.4%; Score 1354; DB 3; Length 394;
Best Local Similarity 99.6%; Pred. No. 2.2e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IIKIVSRNKRKYQEDGFDLDTIYPNIIAMGPPAERLEGVYRNNDVVVFLLDSKHN 60

DB 4 IIKIVSRNKRKYQEDGFDLDTIYPNIIAMGPPAERLEGVYRNNDVVVFLLDSKHN 63

QY 61 HYKIYNLCARHYDTAKNCRVAQYPPEDHNPQLEIKPFCELDQWLSEDDNHVAI 120
 Db 64 HYKIYNLCARHYDTAKNCRVAQYPPEDHNPQLEIKPFCELDQWLSEDDNHVAI 123
 QY 121 CKAGKGRGTGVMICAYLLHKGKFLKAQALDFYGEVTRDKKGVTPSQRRYVYYSYLLK 180
 Db 124 CKAGKGRGTGVMICAYLLHKGKFLKAQALDFYGEVTRDKKGVTPSQRRYVYYSYLLK 183
 QY 181 NHLDRYPVALLFHKKMFETIPMFSGGTGNPQFVVCOLKVKIYSSNSGPTREDKFNYPEF 240
 Db 184 NHLDRYPVALLFHKKMFETIPMFSGGTGNPQFVVCOLKVKIYSSNSGPTREDKFNYPEF 243
 QY 241 POPLPVC 249
 Db 244 POPLPVC 252

RESULT 2

US-09-140-749-17
 ; Sequence 17, Application US/09140749
 ; Patent No. 6482795
 ; GENERAL INFORMATION:
 ; APPLICANT: Steck, Peter
 ; APPLICANT: Pershouse, Mark A.
 ; APPLICANT: Jasser, Samar
 ; APPLICANT: Yung, Alfred W.K.
 ; APPLICANT: Tavtigian, Sean V.
 ; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
 ; FILE REFERENCE: 2318-205
 ; CURRENT APPLICATION NUMBER: US/09/140,749
 ; EARLIER FILING DATE: 1998-08-26
 ; EARLIER APPLICATION NUMBER: U.S. 08/791,115
 ; EARLIER FILING DATE: 1997-01-30
 ; EARLIER APPLICATION NUMBER: U.S. 60/057,750
 ; EARLIER FILING DATE: 1997-08-26
 ; EARLIER APPLICATION NUMBER: U.S. 60/083,563
 ; EARLIER FILING DATE: 1998-04-30
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 17
 ; TYPE: PRT
 ; ORGANISM: Canis familiaris
 US-09-140-749-17

Query Match 99.4%; Score 1354; DB 4; Length 394;
 Best Local Similarity 99.6%; Pred. No. 2.2e-142;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 IIKEIVSRNKRRYQEDGFDLDTIYPNIIAMGFAERLEGVYRNNDVVRFLDSKHKN 60
 Db 4 IIKEIVSRNKRRYQEDGFDLDTIYPNIIAMGFAERLEGVYRNNDVVRFLDSKHKN 63
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 Db 64 HYKIYNLCARHYDTAKNCRVAQYPPEDHNPQLEIKPFCELDQWLSEDDNHVAI 123
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 Db 184 NHLDRYPVALLFHKKMFETIPMFSGGTGNPQFVVCOLKVKIYSSNSGPTREDKFNYPEF 243
 QY 241 POPLPVC 249
 Db 244 POPLPVC 252

RESULT 3

US-08-791-115B-1

; Sequence 1, Application US/08791115B
 ; Patent No. 6262242
 ; GENERAL INFORMATION:
 ; APPLICANT: Steck, Peter
 ; APPLICANT: Pershouse, Mark A.
 ; APPLICANT: Jasser, Samar
 ; APPLICANT: Yung, W.K. Alfred
 ; APPLICANT: Tavtigian, Sean V.
 ; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
 ; STREET: 555 Thirteenth Street, N.W., Suite 701-E
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 22204
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/791,115B
 ; FILING DATE: 30-JAN-1997
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ihnen, Jeffrey L.
 ; REGISTRATION NUMBER: 38,957
 ; REFERENCE/DOCKET NUMBER: 2318-134.A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-683-6040
 ; TELEFAX: 202-683-7031
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 403 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 US-08-791-115B-1

Query Match 99.4%; Score 1354; DB 3; Length 403;
 Best Local Similarity 99.6%; Pred. No. 2.3e-142;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 IIKEIVSRNKRRYQEDGFDLDTIYPNIIAMGFAERLEGVYRNNDVVRFLDSKHKN 60
 Db 4 IIKEIVSRNKRRYQEDGFDLDTIYPNIIAMGFAERLEGVYRNNDVVRFLDSKHKN 63
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 Db 64 HYKIYNLCARHYDTAKNCRVAQYPPEDHNPQLEIKPFCELDQWLSEDDNHVAI 123
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 Db 184 NHLDRYPVALLFHKKMFETIPMFSGGTGNPQFVVCOLKVKIYSSNSGPTREDKFNYPEF 243
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 Db 244 POPLPVC 252

RESULT 4

US-08-791-115B-23
 ; Sequence 23, Application US/08791115B
 ; Patent No. 6262242
 ; GENERAL INFORMATION:
 ; APPLICANT: Steck, Peter
 ; APPLICANT: Pershouse, Mark A.

APPLICANT: Jasser, Samar
APPLICANT: Yung, W.K. Alfred
APPLICANT: Tavtighian, Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,115B
FILING DATE: 30-JAN-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 38,957
REFERENCE/DOCKET NUMBER: 2318-134.A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-683-7031
TELEFAX: 202-683-7031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-115B-23

Query Match 99.4%; Score 1354; DB 3; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F M Y P E F 243
Qy 241 P Q P L P V C G D 249
Db 244 P Q P L P V C G D 252

RESULT 5
US-08-791-115B-25
Sequence 25, Application US/08791115B
Patent No. 6262242
GENERAL INFORMATION:
APPLICANT: Steck, Peter
APPLICANT: Pershouse, Mark A.
APPLICANT: Jasser, Samar
APPLICANT: Yung, W.K. Alfred
APPLICANT: Tavtighian, Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,115B
FILING DATE: 30-JAN-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 38,957
REFERENCE/DOCKET NUMBER: 2318-134.A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-683-7031
TELEFAX: 202-683-7031
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-115B-25

Query Match 99.4%; Score 1354; DB 3; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 4 I I K E I V S N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V V R F L D S K H K N 63
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Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A I H 123
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Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S Q R R Y V Y Y S Y L L K 183
Qy 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F M Y P E F 240
Db 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F M Y P E F 243
Qy 241 P Q P L P V C G D 249
Db 244 P Q P L P V C G D 252

RESULT 6
US-09-140-749-2
Sequence 2, Application US/09140749
Patent No. 6482795
GENERAL INFORMATION:
APPLICANT: Steck, Peter
APPLICANT: Pershouse, Mark A.
APPLICANT: Jasser, Samar
APPLICANT: Yung, Alfred W.K.
APPLICANT: Tavtighian, Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
FILE REFERENCE: 2318-205
CURRENT APPLICATION NUMBER: US/09/140,749
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: U.S. 08/791,115
EARLIER FILING DATE: 1997-01-30
EARLIER APPLICATION NUMBER: U.S. 60/057,750

; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-140-749-2

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
D b 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 180
D b 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 240
D b 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 243
QY 241 P Q P L P V C G D 249
D b 244 P Q P L P V C G D 252

RESULT 7
US-09-140-749-10
; Sequence 10, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtighian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; EARLIER FILING DATE: 1998-08-26
; EARLIER FILING DATE: 1997-01-30
; EARLIER FILING DATE: 1997-08-26
; EARLIER FILING DATE: 1997-08-26
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-140-749-49

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
D b 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 180
D b 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 240
D b 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 243
QY 241 P Q P L P V C G D 249
D b 244 P Q P L P V C G D 252

RESULT 9
US-09-140-749-55
; Sequence 55, Application US/09140749
; Patent No. 6482795

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
D b 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 240
QY 241 P Q P L P V C G D 249
D b 244 P Q P L P V C G D 252

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120

Db 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 180
D b 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 240
D b 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 243
QY 241 P Q P L P V C G D 249
D b 244 P Q P L P V C G D 252

RESULT 8
US-09-140-749-49
; Sequence 49, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtighian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; EARLIER FILING DATE: 1998-08-26
; EARLIER FILING DATE: 1997-01-30
; EARLIER FILING DATE: 1997-01-30
; EARLIER FILING DATE: 1997-08-26
; EARLIER FILING DATE: 1997-08-26
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-140-749-49

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
D b 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 180
D b 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 240
D b 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 243
QY 241 P Q P L P V C G D 249
D b 244 P Q P L P V C G D 252

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
D b 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
D b 64 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 180
D b 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 240
D b 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F 243
QY 241 P Q P L P V C G D 249
D b 244 P Q P L P V C G D 252

RESULT 9
US-09-140-749-55
; Sequence 55, Application US/09140749
; Patent No. 6482795

```
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-140-749-55

Query Match 99.4%; Score 1354; DB 4; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.3e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 60
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 63
QY 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y Y S Y L L K 183
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F N Y F E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S N S G P T R E D K F N Y F E F 243
QY 241 P Q P L P V C G D 249
DB 244 P Q P L P V C G D 252

RESULT 10
US-09-140-749-57
; Sequence 57, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,115B
; FILING DATE: 30-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 38,957
; REFERENCE/DOCKET NUMBER: 2318-134.A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-683-6040
; TELEFAX: 202-683-7031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-791-115B-7
Query Match 99.4%; Score 1354; DB 3; Length 430;
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	Best Local Similarity	99.6%;	Pred. No. 2.5e-142;	Mismatches	Conservative	0;	Gaps	0;
QY	1	I I K E I V S R N K R R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N	60					
Db	40	I I K E I V S R N K R R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N	99					
QY	61	H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P E D H N P Q L E L I K P C E D L D W L S E D D N H V A A I H	120					
Db	100	H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P E D H N P Q L E L I K P C E D L D W L S E D D N H V A A I H	159					
QY	121	C K A G K G R T G V M I C A Y I L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R Y V V Y V Y S Y L L K	180					
Db	160	C K A G K G R T G V M I C A Y I L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R Y V V Y V Y S Y L L K	219					
QY	181	N H L D Y R P V A L L F H K M M F E T I P M F S G G T C N P Q F V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F	240					
Db	220	N H L D Y R P V A L L F H K M M F E T I P M F S G G T C N P Q F V V C O L K V K I Y S S N S G P T R R E D K F N Y F E F	279					
QY	241	P O P L P V C G D	249					
Db	280	P O P L P V C G D	288					

RESULT 12
US-09-140-749-18
; Sequence 18, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-140-749-18

Db 280 PQPLPVCGD 288

|||||

RESULT 13
US-09-140-749-15
; Sequence 15, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140, 749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26

I	I I K E I V S R N K R Y Q E D G F D L J L I I P N I I A M G F P A E R L E G V T R K N N I D D V V R K L D S H K N	60
I I K E I V S R N K R Y Q E D G F D L J L I I P N I I A M G F P A E R L E G V T R K N N I D D V V R K L D S H K N		
40	I I K E I V S R N K R Y Q E D G F D L J L I I P N I I A M G F P A E R L E G V T R K N N I D D V V R K L D S H K N	99
61	H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P E D H N P Q L E L I K P F C E D L O W L S E D D N H V A A I H	120
100	H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P E D H N P Q L E L I K P F C E D L O W L S E D D N H V A A I H	159
121	C K A G K G R T G V M I C A Y L L H R G K F I K A Q E A L D F Y G E V T R D K K G Y T I P S R V V V Y V Y S Y L L K	180
160	C K A G K G R T G V M I C A Y L L H R G K F I K A Q E A L D F Y G E V T R D K K G Y T I P S R V V V Y V Y S Y L L K	219
181	N H L D Y R P V A L L F H K M M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F	240
220	N H L D Y R P V A L L F H K M M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F N Y F E F	279
241	S P L P V C G D	249

RESULT 14
US-08-906-156A-12
; Sequence 12. Application US/08906156A
; Patent No. 6287854
; GENERAL INFORMATION:
; APPLICANT: SPURR, NIGEL K
; APPLICANT: GRAY, IAN C
; APPLICANT: STEWART, LORNA M
; TITLE OF INVENTION: DIAGNOSIS OF SUSCEPTIBILITY TO CANCER
; TITLE OF INVENTION: AND TREATMENT THEREOF
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEEBO ROAD
; CITY: ARLINGTON
; STATE: VA

;; COUNTRY: USA
;; ZIP: 22201
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/906,156A
;; FILING DATE: 05-AUG-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/042,655
;; FILING DATE: 02-APR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/033,147
;; FILING DATE: 13-DEC-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/005,840
;; FILING DATE: 23-OCT-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/96GB/02588
;; FILING DATE: 22-OCT-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SADOFF, B.J.
;; REGISTRATION NUMBER: 36,663
;; REFERENCE/DOCKET NUMBER: 1090-14
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-816-4000
;; TELEFAX: 703-816-4100
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 565 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Translation of partial cDNA sequence
US-08-906-156A-12

Query Match 99.4%; Score 1354; DB 3; Length 565;
Best Local Similarity 99.6%; Pred. No. 3.7e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 60
Db 166 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 225
Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 226 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 285
Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T D K K G V T I P S O R R Y V Y Y S Y L L K 180
Db 286 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T D K K G V T I P S O R R Y V Y Y S Y L L K 345
Qy 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S N S G P T R R E D K F N Y F E F 240
Db 346 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S N S G P T R R E D K F N Y F E F 405
Qy 241 P Q P L P V C G D 249
Db 406 P Q P L P V C G D 414

RESULT 15
US-09-140-749-8
; Sequence 8, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter

;; APPLICANT: Pershouse, Mark A.
;; APPLICANT: Jasser, Samar
;; APPLICANT: Yung, Alfred W.K.
;; APPLICANT: Tavtigan, Sean V.
;; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3
;; FILE REFERENCE: 2318-205
;; CURRENT APPLICATION NUMBER: US/09/140,749
;; CURRENT FILING DATE: 1998-08-26
;; EARLIER APPLICATION NUMBER: U.S. 08/791,115
;; EARLIER FILING DATE: 1997-01-30
;; EARLIER APPLICATION NUMBER: U.S. 60/057,750
;; EARLIER FILING DATE: 1997-08-26
;; EARLIER APPLICATION NUMBER: U.S. 60/083,563
;; EARLIER FILING DATE: 1998-04-30
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 8
;; LENGTH: 597
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-140-749-8
Query Match 99.4%; Score 1354; DB 4; Length 597;
Best Local Similarity 99.6%; Pred. No. 4e-142;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 60
Db 198 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H K N 257
Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 258 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 317
Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T D K K G V T I P S O R R Y V Y Y S Y L L K 180
Db 318 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T D K K G V T I P S O R R Y V Y Y S Y L L K 377
Qy 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S N S G P T R R E D K F N Y F E F 240
Db 378 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V K I Y S N S G P T R R E D K F N Y F E F 437
Qy 241 P Q P L P V C G D 249
Db 438 P Q P L P V C G D 446
Search completed: December 10, 2003, 20:35:42
Job time : 7.16846 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:34:18 ; Search time 11.1032 Seconds
(without alignments)
4170.856 Million cell updates/sec

Title: US-09-205-658A-309
Perfect score: 1362
Sequence: 1 IIKEIVSRNKRYYQEDGDL.....REDKFNFFPQLPVCGD 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1362	100.0	249	9	US-09-205-658-309
2	1362	100.0	249	12	Sequence 309, App
3	1354	99.4	394	12	Sequence 17, Appl
4	1354	99.4	403	10	US-10-299-003-17
5	1354	99.4	403	12	US-09-870-379-2
6	1354	99.4	403	12	US-10-299-003-2
7	1354	99.4	403	12	US-10-299-003-10
8	1354	99.4	403	12	US-10-299-003-49
9	1354	99.4	403	12	US-10-299-003-55
10	1354	99.4	403	12	US-10-299-003-57
11	1354	99.4	403	15	US-10-059-585-50
12	1354	99.4	430	12	US-10-299-003-18
13	1354	99.4	559	12	US-10-299-003-15
14	511	37.5	445	12	US-10-299-003-8
15	494	36.3	645	12	US-10-120-801-101

Sequence 100, App
Sequence 97, Appl
Sequence 57, Appl
Sequence 98, Appl
Sequence 310, App
Sequence 310, App
Sequence 308, App
Sequence 308, App
Sequence 30, Appl
Sequence 37705, A
Sequence 30662, A
Sequence 4, Appl
Sequence 2, Appl
Sequence 31, Appl
Sequence 30, Appl
Sequence 32, Appl
Sequence 2, Appl
Sequence 68, Appl
Sequence 7649, Ap
Sequence 51, Appl
Sequence 613, App
Sequence 18, Appl
Sequence 95, Appl
Sequence 55, Appl
Sequence 51, Appl
Sequence 53, Appl
Sequence 385, App
Sequence 61, Appl
Sequence 57, Appl

664 36.3 494 16
551 35.1 478 17
551 35.1 478 18
551 35.1 478 19
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551 35.1 478 44
551 35.1 478 45

ALIGNMENTS

RESULT 1
US-09-205-658-309
; Sequence 309, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 309
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-309

Query Match 100.0%; Score 1362; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.1e-134;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 I I K E I V S R N K R Y Q E D G D L T Y I P N I I A M G P F A E R L E G V Y R N I D D V R F L D S K H K N 60
DB 1 I I K E I V S R N K R Y Q E D G D L T Y I P N I I A M G P F A E R L E G V Y R N I D D V R F L D S K H K N 60
QY 61 H Y K I Y N L C A E R H Y T A F N C H V A Q Y P F E D H N P P Q L E I K P C E D L D Q W L S E D D N H V A I H 120
DB 61 H Y K I Y N L C A E R H Y T A F N C H V A Q Y P F E D H N P P Q L E I K P C E D L D Q W L S E D D N H V A I H 120

QY 121 CKAGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKKGVTTIPSORRYVYYSYLLK 180
DB 121 CKAGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKKGVTTIPSORRYVYYSYLLK 180
QY 181 NHDYRPVALLPHKMFETIPMFSGTGNPQFVVCQKVKIYSSNSGPTREDKFNYPEF 240
DB 181 NHDYRPVALLPHKMFETIPMFSGTGNPQFVVCQKVKIYSSNSGPTREDKFNYPEF 240
QY 241 POPLPVCGD 249
DB 241 POPLPVCGD 249

RESULT 2

US-09-963-693-309
; Sequence 309, Application US/09963693
; Publication No. US20030181364A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Osg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963,693
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/205,658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/857,076
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: 08/888,534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US98/10080
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 309
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans

US-09-963-693-309

Query Match 100.0%; Score 1362; DB 12; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.1e-134;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIKEIVSRNKRKYQEDGFDLDTIYYPNIAMGPPAERLEGVYRNNDVVRFLDSKHN 60
DB 1 IIKEIVSRNKRKYQEDGFDLDTIYYPNIAMGPPAERLEGVYRNNDVVRFLDSKHN 60
QY 61 HYKIYNLCARHYDTAKNCRVAQYPPFDHNPPOLELIKPFCELDQWLSDDNHVAIH 120
DB 61 HYKIYNLCARHYDTAKNCRVAQYPPFDHNPPOLELIKPFCELDQWLSDDNHVAIH 120
QY 121 CKAGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKKGVTTIPSORRYVYYSYLLK 180
DB 121 CKAGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKKGVTTIPSORRYVYYSYLLK 180
QY 181 NHDYRPVALLPHKMFETIPMFSGTGNPQFVVCQKVKIYSSNSGPTREDKFNYPEF 240
DB 181 NHDYRPVALLPHKMFETIPMFSGTGNPQFVVCQKVKIYSSNSGPTREDKFNYPEF 240
QY 241 POPLPVCGD 249
DB 241 POPLPVCGD 249

RESULT 3

US-10-299-003-17
; Sequence 17, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.

; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-299-003-17

Query Match 99.4%; Score 1354; DB 12; Length 394;

Best Local Similarity 99.6%; Pred. No. 1.4e-133;

Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IIKEIVSRNKRKYQEDGFDLDTIYYPNIAMGPPAERLEGVYRNNDVVRFLDSKHN 60
DB 4 IIKEIVSRNKRKYQEDGFDLDTIYYPNIAMGPPAERLEGVYRNNDVVRFLDSKHN 63
QY 61 HYKIYNLCARHYDTAKNCRVAQYPPFDHNPPOLELIKPFCELDQWLSDDNHVAIH 120
DB 64 HYKIYNLCARHYDTAKNCRVAQYPPFDHNPPOLELIKPFCELDQWLSDDNHVAIH 123
QY 121 CKAGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKKGVTTIPSORRYVYYSYLLK 180
DB 124 CKAGKRTGVMICAYLLHKGKFLKQAEALDFGEVTRDKKGVTTIPSORRYVYYSYLLK 183
QY 181 NHDYRPVALLPHKMFETIPMFSGTGNPQFVVCQKVKIYSSNSGPTREDKFNYPEF 240
DB 184 NHDYRPVALLPHKMFETIPMFSGTGNPQFVVCQKVKIYSSNSGPTREDKFNYPEF 243
QY 241 POPLPVCGD 249
DB 244 POPLPVCGD 252

RESULT 4

US-09-870-379-2
; Sequence 2, Application US/09870379
; Patent No. US20020150954A1
; GENERAL INFORMATION:
; APPLICANT: Donald L. Durden
; APPLICANT: ADVANCED RESEARCH & TECHNOLOGY INSTITUTE
; TITLE OF INVENTION: Compositions and Methods for Identifying
; FILE REFERENCE: ARTI 0024-US
; CURRENT APPLICATION NUMBER: US/09/870,379
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17358
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/274/167
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/208,437
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-870-379-2

Query Match 99.4%; Score 1354; DB 10; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F M Y E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F M Y E F 243

QY 241 P Q P L P V C G D 249
DB 244 P Q P L P V C G D 252

RESULT 5
US-10-299-003-2
; Sequence 2, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigan, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-299-003-2

Query Match 99.4%; Score 1354; DB 12; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F M Y E F 240

DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F M Y E F 243

QY 241 P Q P L P V C G D 249
DB 244 P Q P L P V C G D 252

RESULT 6
US-10-299-003-10
; Sequence 10, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigan, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-299-003-10

Query Match 99.4%; Score 1354; DB 12; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M F P A E R L E G Y V R N N I D D V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F M Y E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V V C Q L K V K I Y S S N S G P T R R E D K F M Y E F 243

QY 241 P Q P L P V C G D 249
DB 244 P Q P L P V C G D 252

RESULT 7
US-10-299-003-49
; Sequence 49, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigan, Sean V.

;; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
;; FILE REFERENCE: 2318-385
;; CURRENT APPLICATION NUMBER: US/10/299,003
;; CURRENT FILING DATE: 2002-11-19
;; PRIOR APPLICATION NUMBER: U.S. 09/140,749
;; PRIOR FILING DATE: 1998-08-26
;; PRIOR APPLICATION NUMBER: U.S. 08/791,115
;; PRIOR FILING DATE: 1997-01-30
;; PRIOR APPLICATION NUMBER: U.S. 60/057,750
;; PRIOR FILING DATE: 1997-08-26
;; PRIOR APPLICATION NUMBER: U.S. 60/083,563
;; PRIOR FILING DATE: 1998-04-30
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 49
;; LENGTH: 403
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-10-299-003-49

Query Match 99.4%; Score 1354; DB 12; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	IIKEIVSRNKRRYQEDGFDLDLTIIYPNIIAMGFAERLEGVYRNNDVVRFDSKHN	60
Db	4	IIKEIVSRNKRRYQEDGFDLDLTIIYPNIIAMGFAERLEGVYRNNDVVRFDSKHN	63
Qy	61	HYKIYNLCAERHYDTAKFNCRAQVPPFDHNPPOLELIKPFCELDQWLSEDDNHVAI	120
Db	64	HYKIYNLCAERHYDTAKFNCRAQVPPFDHNPPOLELIKPFCELDQWLSEDDNHVAI	123
Qy	121	CKAGKRTGVNMCAYLLHGRGKFLKAQALDPYGEVTRDKKGVTPSORRYVYYSYLLK	180
Db	124	CKAGKRTGVNMCAYLLHGRGKFLKAQALDPYGEVTRDKKGVTPSORRYVYYSYLLK	183
Qy	181	NHLDYRPVALLFHKMPETIPMFSGTCNPQFVVCOLKVKIYSSNSGPTREDKFNYPEF	240
Db	184	NHLDYRPVALLFHKMPETIPMFSGTCNPQFVVCOLKVKIYSSNSGPTREDKFNYPEF	243
Qy	241	PQPLPVCGD 249	
Db	244	PQPLPVCGD 252	

RESULT 8

US-10-299-003-55
;; Sequence 55, Application US/10299003
;; Publication No. US20030139324A1
;; GENERAL INFORMATION:
;; APPLICANT: Steck, Peter
;; APPLICANT: Pershouse, Mark A.
;; APPLICANT: Jasser, Samar
;; APPLICANT: Yung, Alfred W.K.
;; APPLICANT: Tavtigan, Sean V.
;; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
;; FILE REFERENCE: 2318-385
;; CURRENT APPLICATION NUMBER: US/10/299,003
;; CURRENT FILING DATE: 2002-11-19
;; PRIOR APPLICATION NUMBER: U.S. 09/140,749
;; PRIOR FILING DATE: 1998-08-26
;; PRIOR APPLICATION NUMBER: U.S. 08/791,115
;; PRIOR FILING DATE: 1997-01-30
;; PRIOR APPLICATION NUMBER: U.S. 60/057,750
;; PRIOR FILING DATE: 1997-08-26
;; PRIOR APPLICATION NUMBER: U.S. 60/083,563
;; PRIOR FILING DATE: 1998-04-30
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 55
;; LENGTH: 403
;; TYPE: PRT
;; ORGANISM: Canis familiaris

US-10-299-003-55

Query Match 99.4%; Score 1354; DB 12; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	IIKEIVSRNKRRYQEDGFDLDLTIIYPNIIAMGFAERLEGVYRNNDVVRFDSKHN	60
Db	4	IIKEIVSRNKRRYQEDGFDLDLTIIYPNIIAMGFAERLEGVYRNNDVVRFDSKHN	63
Qy	61	HYKIYNLCAERHYDTAKFNCRAQVPPFDHNPPOLELIKPFCELDQWLSEDDNHVAI	120
Db	64	HYKIYNLCAERHYDTAKFNCRAQVPPFDHNPPOLELIKPFCELDQWLSEDDNHVAI	123
Qy	121	CKAGKRTGVNMCAYLLHGRGKFLKAQALDPYGEVTRDKKGVTPSORRYVYYSYLLK	180
Db	124	CKAGKRTGVNMCAYLLHGRGKFLKAQALDPYGEVTRDKKGVTPSORRYVYYSYLLK	183
Qy	181	NHLDYRPVALLFHKMPETIPMFSGTCNPQFVVCOLKVKIYSSNSGPTREDKFNYPEF	240
Db	184	NHLDYRPVALLFHKMPETIPMFSGTCNPQFVVCOLKVKIYSSNSGPTREDKFNYPEF	243
Qy	241	PQPLPVCGD 249	
Db	244	PQPLPVCGD 252	

RESULT 9

US-10-299-003-57
;; Sequence 57, Application US/10299003
;; Publication No. US20030139324A1
;; GENERAL INFORMATION:
;; APPLICANT: Steck, Peter
;; APPLICANT: Pershouse, Mark A.
;; APPLICANT: Jasser, Samar
;; APPLICANT: Yung, Alfred W.K.
;; APPLICANT: Tavtigan, Sean V.
;; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
;; FILE REFERENCE: 2318-385
;; CURRENT APPLICATION NUMBER: US/10/299,003
;; CURRENT FILING DATE: 2002-11-19
;; PRIOR APPLICATION NUMBER: U.S. 09/140,749
;; PRIOR FILING DATE: 1998-08-26
;; PRIOR APPLICATION NUMBER: U.S. 08/791,115
;; PRIOR FILING DATE: 1997-01-30
;; PRIOR APPLICATION NUMBER: U.S. 60/057,750
;; PRIOR FILING DATE: 1997-08-26
;; PRIOR APPLICATION NUMBER: U.S. 60/083,563
;; PRIOR FILING DATE: 1998-04-30
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 57
;; LENGTH: 403
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-10-299-003-57

Query Match 99.4%; Score 1354; DB 12; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	IIKEIVSRNKRRYQEDGFDLDLTIIYPNIIAMGFAERLEGVYRNNDVVRFDSKHN	60
Db	4	IIKEIVSRNKRRYQEDGFDLDLTIIYPNIIAMGFAERLEGVYRNNDVVRFDSKHN	63
Qy	61	HYKIYNLCAERHYDTAKFNCRAQVPPFDHNPPOLELIKPFCELDQWLSEDDNHVAI	120
Db	64	HYKIYNLCAERHYDTAKFNCRAQVPPFDHNPPOLELIKPFCELDQWLSEDDNHVAI	123
Qy	121	CKAGKRTGVNMCAYLLHGRGKFLKAQALDPYGEVTRDKKGVTPSORRYVYYSYLLK	180
Db	124	CKAGKRTGVNMCAYLLHGRGKFLKAQALDPYGEVTRDKKGVTPSORRYVYYSYLLK	183

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Qy 181 NHDYRPVALLPHKMFETIPMFSGTCNPQVVCOLKVKIYSSNSGTRREDKFNYPEF 240
Db 184 NHDYRPVALLPHKMFETIPMFSGTCNPQVVCOLKVKIYSSNSGTRREDKFNYPEF 243

Qy 241 POPLPVCGD 249
Db 244 POPLPVCGD 252

RESULT 10
US-10-059-585-50
; Sequence 50, Application US/10059585
; Publication No. US2003008276A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Senoo, Chaki
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-50

Query Match 99.4%; Score 1354; DB 15; Length 403;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N 60
Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N 63

Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 64 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123

Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
Db 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 183

Qy 181 N H L D Y R P V A L L P H K M F E T I P M F S G T C N P Q V V C O L K V K I Y S S N S G T R R E D K F N Y P E F 240
Db 184 N H L D Y R P V A L L P H K M F E T I P M F S G T C N P Q V V C O L K V K I Y S S N S G T R R E D K F N Y P E F 243
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Qy 241 POPLPVCGD 249
Db 244 POPLPVCGD 252

RESULT 11
US-10-299-003-18
; Sequence 18, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-299-003-18

Query Match 99.4%; Score 1354; DB 12; Length 430;
Best Local Similarity 99.6%; Pred. No. 1.6e-133;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N 60
Db 40 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H N 99

Qy 61 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 100 H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 159

Qy 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 180
Db 160 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y V Y Y S Y L L K 219

Qy 181 N H L D Y R P V A L L P H K M F E T I P M F S G T C N P Q V V C O L K V K I Y S S N S G T R R E D K F N Y P E F 240
Db 220 N H L D Y R P V A L L P H K M F E T I P M F S G T C N P Q V V C O L K V K I Y S S N S G T R R E D K F N Y P E F 279

Qy 241 POPLPVCGD 249
Db 280 POPLPVCGD 288

RESULT 12
US-10-299-003-15
; Sequence 15, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
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Search completed: December 10, 2003, 20:43:25
Job time : 12.1032 secs

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/ FILE REFERENCE: 2102-340
/ CURRENT APPLICATION NUMBER: US/10/120,801
/ CURRENT FILING DATE: 2002-04-11
/ PRIOR APPLICATION NUMBER: 60/285748
/ PRIOR FILING DATE: 2001-04-23
/ PRIOR APPLICATION NUMBER: 60/286068
/ PRIOR FILING DATE: 2001-04-24
/ PRIOR APPLICATION NUMBER: 60/286292
/ PRIOR FILING DATE: 2001-04-25
/ PRIOR APPLICATION NUMBER: 60/288334
/ PRIOR FILING DATE: 2001-05-03
/ PRIOR APPLICATION NUMBER: 60/291241
/ PRIOR FILING DATE: 2001-05-16
/ PRIOR APPLICATION NUMBER: 60/322284
/ PRIOR FILING DATE: 2001-09-14
/ PRIOR APPLICATION NUMBER: 60/285609
/ PRIOR FILING DATE: 2001-04-20
/ NUMBER OF SEQ ID NOS: 155
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 101
/ LENGTH: 645
/ TYPE: PRT
/ ORGANISM: mouse
/ US-10-120-801-101

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Query Match      36.3%; Score 494; DB 12; Length 645;
Best Local Similarity 48.8%; Pred. No. 5.3e-43;
Matches 99; Conservative 36; Mismatches 60; Indels 8; Gaps 3;

Qy 1 I I K E I V R N K R R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N I D D V V R F L D S K H K N 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 319 L T R K L V G N K R R Y K D G F D L D L T Y V T E R I I A M S F P S G R E S F Y R N P I K E V V R F L D T K H P N 378

Qy 61 H Y K I Y N I C A E R H Y T A K P N C R V A Q Y P E D H N P P O L E I K P C E D L D W L S E D D N H V A A I H 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 379 H Y O Y N I C S E R A Y Q P K F H Y V R V R I M I D D H N V P T L E E M L L F S K V N N M A O D P E N N V A I H 438

```

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:30:07 ; Search time 7.19653 Seconds
(without alignments)
3327.436 Million cell updates/sec

Title: US-09-205-658A-309

Perfect score: 1362

Sequence: 1 IIKKIVSRNKRKYQEDGFDL.....RREDKFNFFPQPLPVCGD 249

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	514.5	37.8	628	2 T45864	probable tyrosine
2	465	34.1	962	2 T51924	daf-18 protein - C
3	465	34.1	965	2 T32574	hypothetical prote
4	328	24.1	1744	2 A54970	tensin, cardiac mu
5	328	24.1	1792	2 A57075	tensin - chicken
6	317.5	23.3	1733	2 S27939	tensin - chicken
7	309	22.7	348	2 T40573	protein-tyrosine p
8	286	21.0	1305	2 T31096	cyclin G-associate
9	265	19.5	910	2 S68983	auxilin - bovine
10	244	17.9	434	2 S55155	probable tyrosine
11	187	13.7	264	2 T25762	hypothetical prote
12	144	10.6	537	2 T50099	probable protein-t
13	129	9.5	551	2 S56283	protein-tyrosine-p
14	121.5	8.9	173	2 A56059	protein-tyrosine-p
15	120	8.8	802	1 B44390	protein-tyrosine-p
16	115	8.4	171	1 B47452	dual specificity p
17	111.5	8.2	167	2 J55981	prenylated protein
18	110	8.1	171	1 I36845	dual specificity p
19	110	8.1	171	2 T28522	probable dual spec
20	110	8.1	171	2 B72161	JIL protein - vari
21	110	8.1	1897	1 T0HULK	leukocyte antigen-
22	109	8.0	171	1 QQVZH1	dual specificity p
23	109	8.0	171	1 A42514	dual specificity p
24	108.5	8.0	154	2 I68523	protein tyrosine p
25	108.5	8.0	173	2 J55982	prenylated protein
26	108.5	8.0	190	2 T43172	probable protein-t
27	106	7.8	446	2 T33986	hypothetical prote
28	102	7.5	582	2 A57068	protein-tyrosine-p
29	102	7.5	1290	2 A56493	leucocyte common a

30 100.5 7.4 742 2 F84643
31 100.5 7.4 829 1 A47373
32 100.5 7.4 2302 2 T14328
33 99.5 7.3 394 2 A56115
34 99.5 7.3 796 1 JCL1285
35 99 7.3 668 2 T34317
36 98.5 7.2 218 2 T01111
37 98.5 7.2 802 1 A36085
38 98.5 7.2 1409 2 T42522
39 97 7.1 543 2 AB0850
40 97 7.1 1898 2 S46216
41 96.5 7.1 780 1 JCL1368
42 96 7.0 168 1 A40781
43 94 6.9 1912 2 A56178
44 94 6.9 2029 1 TDFFLK
45 93 6.8 681 2 E88158

ALIGNMENTS

RESULT 1

T45864

Probable tyrosine phosphatase - Arabidopsis thaliana

k;Alternate names: protein F3A4.190

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C;Accession: T45864

R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May

submitted to the Protein Sequence Database, December 1999

A;Reference number: 223007

A;Accession: T45864

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-628 <BAR>

A;Cross-references: EMBL:AL132978

A;Experimental source: cultivar Columbia; BAC clone F3A4

C;Genetics:

A;Map position: 3

A;Introns: 192/3; 226/3; 245/3; 267/3; 326/3; 355/3; 377/2; 399/1; 414/3; 458/2; 481/3

A;Note: F3A4.190

Query Match 37.8%; Score 514.5; DB 2; Length 628;

Best Local Similarity 50.0%; Pred. No. 1.1e-38;

Matches 95; Conservative 36; Mismatches 50; Indels 9; Gaps 2;

Qy 3 KEIVSRNKRKYQEDGFDLDTIYIPNIAMGFAERL-----EGVVRNNDVVRF 54

Db 181 RHIVSQNRKRYQEGFDLDTIYITENIAMGFPAGDISGSLGFGFEGLYRNHMEVIRKF 240

Qy 55 DSKHNHYKIYNLCARHYDTAKENCRAVQYFFEDHNPPLQELIKPFCEDLDLSEDDN 114

Db 241 ETHHKDKYKYNLCSERLYDASREFGKVASFPFDHNCPPQLIPSCFSAYTWLKEDIQ 300

Qy 115 HVAIHAKAGRTGVNMCAYLLHRGFLKAQALDFYGEVTRDKKGVITPSQRYVY 174

Db 301 NVVVHCKAGNARTGLMCLLLYKFPPTAEAEIDYNNQKRCLDGKALVLPSTQIRYVKY 360

Qy 175 YSYLLKNHLD 184

Db 361 YE-RVQNQFD 369

RESULT 2

T51924

daf-18 protein - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

C;Accession: T51924

R;Ogg, S.; Ruvkun, G.

Mol. Cell 2, 887-893, 1998

A;Title: The C. elegans PTEN homolog DAF-18 acts in the insulin receptor-like metabolic

A;Reference number: 225864

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Query Match      34.1%; Score 465; DB 2; Length 965;
Best Local Similarity 41.2%; Pred.No.5.9e-34;
Matches 93; Conservative 38; Mismatches 85; Indels 10; Gaps 2;

Qy    1 I I K E I V S R N K R R Y C D G F D L D T Y I P N I A M G P P A E R L E G V Y R N N I D D V V U F L D S K H - K   59
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Db    48 I F T A V S N R C R T E Y Q N I D L D C A I I T O R I A I G Y P A T G I E A N F N S K V O C Q F L T R H G K   107

Qy    60 N H Y K I Y N L C A B R H Y D T A K E N C R V A Q Y F E D H N P P Q L E I I K F P C S D L D Q W L S E D D N H V A A I   119
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    108 G N V K V F N L R G G Y Y D A D N F D G N V I C F M O T D H H P S E L M A P F C R E A K E W L E A D D K H V I A V   167

Qy    120 H C K A G K R T G W I C A Y I L L R H R G K F I A Q E A L D F Y G E V T R D K K G V T I P S Q R R Y V V Y Y S L L   179
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    168 H C K A G K R T G W I C A L L I Y I N F Y P S P R Q I L D Y S I I R T K N K G V T I P S Q R R Y I Y Y H K L R   227

Qy    180 K N H L D Y P V A L L F K H M F E T I P M F S G G T C N D Q F V V C O L K V I Y S N   225
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    228 E R E N I Y L P L R M Q L I G V Y V E R P P K T W G G S -----K I K V E V G N   264

RESULT 4
A54970
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Query Match      24.1%; Score 328; DB 2; Length 1792;
Best Local Similarity 33.8%; Pred. No. 3.4e-21;
Matches 72; Conservative 45; Mismatches 92; Indels 4; Gaps 3;

Qy 15 EDGFDDLTYINIIAMGPFARLEGVYRNNDVVVFLDSKQKHXYKYNICAERHYD 74
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 110 ESCELDLVYITRIITAVSPSTAECOSPSRNLREVAHMLKSHGDNVYLFNI--SERHD 168
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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A:Gene: SPAC609.02
A:Map position: 2
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	Query Match Best Local Similarity Matches	22.7% 37.2%; Pred No.' 2.4e-20; Conservative	Score 309; DB 2; Mismatches 75;	Length 348; Indels 8; Gaps
QY	1	I I K E I V S R N K R R Y Q E D G F D - - - L D T Y I Y P N I A M G F P A E R L E G V Y R N R I D D V V R F I D	55	
D b	3	I L R V S R G R K G L Q K X W N R S F A Y L D M V Y I T S K V I A M S T P A A C I H K L Y R N D E L D V F K Y L T	62	
QY	56	S K H K H N Y K I Y N L C A E R H - Y D T A K E N C E V A Q Y P E D H N P P Q L E L I K F C E D L D W L S E D D N	114	
D b	63	T O L A D N W I L L N L C A B E T V Y H L E U F K P N I V N Y G F D H N P P P L L F L W A I V M N M D A L F O T Q P L	122	
QY	115	H V A A I H C A G K G R T G V M I C A Y L L H R G K F L Q A O A L D F Y G E V R T R D K G G V T I P S Q R R Y V Y	174	
D b	123	L T L V H V C A G K G R T G T V I C S Y L V A F G - U T A K Q S L E Y T E K M V R G H G I T I S S Q I R Y V Y	181	
QY	175	Y S Y L L K N H D Y	185	
D b	182	I E - I L K O F P N Y	191	

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03 IQKADNLLGNWCAGEIVIHDEUFKNVNIINGQKDNFFPEFLFDMALVINMUALFQIQPF 142
QY      115 HVAATHCKAGKGRGTGVNMICAYLLHHRGFKLKAQBALDPYGEVTRDRDKKGVTTIPSSRRYYVY 174
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      123 LTLVVHCAGKAGRTGTVCISYLVAFGG-LTAKQSLELYTEKMVRGHGLTISSIRYYVY 181
QY      175 YSYLLKNHLDY 185
       :|||:
Db      182 IE-ILKQFPNY 191

RESULT 8
Cyclin G-associated kinase GAK - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C.Accession: T3l096
R.Kanaoka, Y.; Kimura, S.H.; Okazaki, I.; Ikeda, M.; Nojima, H.
FEBS Lett. 402, 73-80, 1997
A.Title: GAK: a cyclin G-associated kinase contains a tensin/auxilin-like domain
A.Reference number: J20979; MUID:97165969; PMID:9013862
A.Accession: T3l096
A.Status: preliminary; translated from GE/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-1305 <KAN>
A.Cross-references: EMBL:D38560; NID:g1902912; PIDN:BAA18911.1; PID:g1902913
A.Note: GAK and cyclin G associated together in vivo
C.Genetics:
A.Gene: GAK

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A>Status: preliminary; translated from GE/EMBL/DDSU
A:Molecule type: mRNA
A:Residues: 1-1305 <KAN>
A:Cross-references: EMBL:D38560; NID:g1902912; PIDN:BAA18911.1; PID:g1902913
A>Note: GAK and cyclin G associate together in vivo
C:Genetics:
A:Gene: GAK

	Query Match	21.0%	Score 286;	DB 2;	Length 1305;
	Best Local Similarity	32.2%;	Pred. No. 1.5e-17;		
	Matches	67;	Conservative	36;	Mismatches 87; Indels 18; Gaps 7
QY	19	LDLITYTPNIAGFPAERLEGVRYRNNIDVDVRFLLDSKHKNHYKYNLCAEHRHYDTAF	78		
Db	405	DLDISYTSRTAVMSFPAEGVESAKNNIEDVLFLDAKHPGYAYNLSPRIYRASPF	463		
QY	79	NCRVAQYPFDNDHNPPLQLIKPCEDDLDWLSBDDNHVAAIHCAGKGRTGVMICAYLLH	138		
		:::::	:::::	:::::	:::::
Db	464	HNRVTECGWVRRAPHLSLYTLCSRHAWLRHDHNVCVVHCMDGRAASAVCAFLCF	523		
		:::::	:::::	:::::	:::::
QY	139	RGKFLKAQEAALDFYGEVRTDKGVTIPSORRVYYYSYLKKHLDYRPVA-----LLFH	193		
		:::::	:::::	:::::	:::::
Db	524	CRLFTSEAAAYMFS--MKRCPPGIW-PSHKRIEYVCDMAVE---EPITHSKMPLVK	576		
		:::::	:::::	:::::	:::::
QY	194	KMFETTPMES--GGTCNPOFVVCQLKV	219		
		:::::	:::::	:::::	:::::
Db	577	SWMTPTVPFLFSKQRNGCRP---FCEVYV	601		

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00      194  KMPETIPMFSS--GGTCNPQFVVCQLKV 219
01      :::::|:::|
02      Db  577  SWVTVPVLFKQKRGCRP---FCEVVV 601
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A:Reference number: S68983; MUID:95220355; PMID:7705342
A:Accession: S68983
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-910 <SCH>
A:Cross-references: EMBL:U09237; NID:G485268; PIDN:AAA79037.1; PID:G485269
A:Superfamily: dnaJ amino-terminal homology
F:846-910/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 19.5%; Score 265; DB 2; Length 910;
Best Local Similarity 28.8%; Pred. No. 7.7e-16;
Matches 66; Conservative 46; Mismatches 99; Indels 18; Gaps 7;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G P A E R L - E G V Y R N N I D D V R F L D S K H 60
DB 49 V I Q S T S Y T K G - - - - - D L D T Y T S R I I V N S F P L D S V D I G R N Q V D D I R S F L D S R H L D 101

QY 61 H Y K I V N L C A E R H Y D T A K F N C R V A Q P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A A I H 120
DB 102 H T V T N L - S P K S Y R T A K F H S R V S E C S W P I R Q A P S L H N L F A V C R N M Y N W L L Q N P K N V C V H 160

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I - P S Q R R Y V Y Y S Y L L 179
DB 161 C L D G R A A S S I L V G A M F I C N L Y S T P C P A V - - - - - R L L Y A K R P G I G L S P S H R R Y L G Y M C D L L 216

QY 180 K N H L D Y R P - V A L L F H K M F E T I P M P S - - - G G T C N F Q F V C Q L K V K I Y S S 224
DB 217 A D K - P Y R P H K F L T I K S I T V S P V P F N K O R N C R E Y C D V L I G E T K I Y T T 264

RESULT 10
S55155
probable tyrosine phosphatase YNL128w - yeast (Saccharomyces cerevisiae)
N:Alternate names: probable tyrosine phosphatase N1220; protein JTB434; protein N1872
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence revision 01-Sep-1995 #text_change 21-Jul-2000
C:Accession: S55155; S59260; S63073
R:Mallet, L.; Bussiereau, F.; Jacquet, M.
A:Description: A 43.5 kb fragment of the chromosome XIV.
A:Reference number: S55136
A:Accession: S55155
A:Molecule type: DNA
A:Residues: 1-434 <MAL>
A:Cross-references: EMBL:246843; NID:G861113; PID:G854509
R:Mallet, L.; Bussiereau, F.; Jacquet, M.
Yeast 11, 1195-1209, 1995
A:Title: A 43.5 kb segment of yeast chromosome XIV, which contains MFA2, MEP2, CAP/SRV2,
A:Reference number: S59241; MUID:96109932; PMID:8619318
A:Accession: S59260
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-434 <MAV>
A:Cross-references: EMBL:246843; NID:G861113; PIDN:CAA86897.1; PID:G854509
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994
R:Mallet, L.; Bussiereau, F.; Jacquet, M.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63069
A:Accession: S63073
A:Molecule type: DNA
A:Residues: 1-434 <MAF>
A:Cross-references: EMBL:271404; NID:gl302063; PID:e239804; PID:gl302064; MIPS:YNL128w
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:TEP1
A:Cross-references: SGD:S005072; MIPS:YNL128w
A:Map position: 14L
C:Keywords: transmembrane protein
F:38-54/Domain: transmembrane #status predicted <TML>

Query Match 17.9%; Score 244; DB 2; Length 434;
Best Local Similarity 27.6%; Pred. No. 2.5e-14;
Matches 66; Conservative 41; Mismatches 64; Indels 68; Gaps 9;

1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G P A E R L - E G V Y R N N I D D V R F L D S K H 58
22 L M K K I L S L P M K K T K N D I G L R L D I S Y I L V N L I V C S Y P V N T Y P K L L Y R N S L D L I L F L T V Y H 81
59 - K N H K I V N L C A E R H Y D T A K F N - - - - - C R V A Q P P F E - - - - - 88
82 G K G N F I P N F R G E K E D S D Y K D N D L I G I T A A K F E S K D F E I Q E L R S T L I N D K I P I S P I D L E T 141
89 - - - - - D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A A I H C K A G K R T G 129
142 R T L V E E T N N V I C E R I G W L D H F P P F E L L E B I V D G I E N Y L S V S K R V A V L H C R M G K G R S G 201
130 V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R - - - - - T R D K - - - - - K G V T I P S Q R R Y V Y Y S Y L L 179
202 M I T W A Y L M - - - - - K Y L Q C P - - - - - L G E A R L I F M Q A R F K Y G M T G V T I P S Q L R Y L R V H E F F I 252

RESULT 11
T25762
hypothetical protein F46F11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25762
R:Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid F46F11.
A:Reference number: Z20083
A:Accession: T25762
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-264 <PAU>
A:Cross-references: EMBL:U88173; PIDN:AAB42265.1; GSPDB:GN00019; CESP:F46F11.3
A:Experimental source: strain Bristol N2; clone F46F11
C:Genetics:
A:Gene: CESP:F46F11.3
A:Map position: 1
A:Introns: 21/3; 43/1; 75/3; 154/2; 182/2; 234/2

Query Match 13.7%; Score 187; DB 2; Length 264;
Best Local Similarity 21.9%; Pred. No. 2e-09;
Matches 56; Conservative 56; Mismatches 120; Indels 24; Gaps 7;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G P A E R L E G V Y R N N I D D V R F L D S K H N 60
DB 15 L V E K L R R K Q K M D R K E G V Q V E - - Y I T R L I V L S C T S E T S E R K F V E S L L K A S Q I Q N A H N K 72
QY 61 H Y K I V N L C A E R H Y D T A K F N C R V A Q P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A A I H 120
DB 73 H I R V N V S Q R R H D I S S L D A I P F G W P S E - - T A P S L E K L C T I C K N L D Q M L E H P L N I A V I F 130

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K - - - - - K G V T I P S Q R R Y V Y Y S 176
DB 131 C K G G L E R C A I V V N A F M R F N A I S A T D D S V D D R F S Q R F S E R F L G P D G P - - P S Y K R Y L G Y F S 188

QY 177 Y L L K N H L D Y R P V A L L F H K M - - - - - F E T I P M F S G G T C N F Q F V C Q L K V K I Y S S N S G T R E D 233
DB 189 S L L S G R I S V N S D P L Y L H N I L T F F E P I N V F - - - - - L K I Y E R L V P V Y Q S T K V A L N K S S 240

QY 234 K F N V F E F P Q P L P V C G D 249
DB 241 K - - - - F E M D G S L K R G D 253

RESULT 12
T50099
probable protein-tyrosine phosphatase CDC14 homolog [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: T50099
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
submitted to the EMBL Data Library, February 2000
A:Reference number: Z25037

A;Reference number: S62230
A;Accession: S62239.
A;Molecule type: DNA
A;Residues: 1-551 <WUV>
A;Cross-references: EMBL:D44602; NID:g893419; PID:d1008630; PID:g893423
R;Ski, T.; Naitou, M.; Hagiwara, H.; Abe, M.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; T
Yeast 12, 177-190, 1996
A;Title: Fifteen open reading frames in a 30.8 kb region of the right arm of chromosome
A;Reference number: S63830; MUID:96287654; PMID:8686381
A;Accession: S63833
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-551 <EKI>
A;Cross-references: EMBL:D44602; NID:g893419; PID:d1008630; PID:g893423
R;Shirayama, M.; Matsui, Y.; Toh-e, A.
Mol. Gen. Genet. 251, 176-185, 1996
A;Title: Dominant mutant alleles of yeast protein kinase gene CDC15 suppress the Ite1 d
A;Reference number: S69234; MUID:96242150; PMID:8668128
A;Accession: S69234
A;Molecule type: DNA
A;Residues: 1-117,'P',119-551 <SHI>
A;Cross-references: EMBL:D57515; NID:g870755; PIDN:BAA09533.1; PID:g870756
C;Genetics:
A;Gene: SGD:CDC14
A;Cross-references: SGD:S0001924; MIPS:YFR028C
A;Map position: 6R
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;283/Active site: Cys (phosphocysteine intermediate) #status predicted
F;289/Binding site: substrate phosphate (Arg) #status predicted

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Best Local Similarity 26.3%; Pred. NO. 0.00032;
Matches 50; Conservative 68; Indels 46; Gaps 9;

QY      7 SRNRRYQEDGDLDTIYPNIIAMGFAER-----LEGVYRNN 46
Db      : | | | | | | | | | | | | | | | | | | | |
166 SYEKYEHVEFG---DFNLTDPDFAASQEDHPKGYLATKSSHLNQPPKSVLNFANN 222
QY      47 IDVVRFLDSK--HKNHKYIYNLCARHYVDYTKAFNCRCVAQYPPEDHNPPOLELIPKPCD 104
Db      : | | | | | | | | | | | | | | | | | | | |
223 VOLVVR-LNSHLYNKKHFDIGI---QHLDLI-----FEDGTCPLDSIVKNEVGA 268
QY      105 LDOWLSEDDNHVAAIHCKAGKGTGVMICAYLLHRGKFLKQAQALDFYGVRRTRDKKGV 164
Db      : | | | | | | | | | | | | | | | | | | | |
269 AETIIIRKGGK--IAVHCKAGLGRGTGLGAHLIYTYGF-TANECIGFLREIR---PGMV 321
QY      165 IPSORRYVYVY 175
Db      : | | | | | | | | | | | | | | | | | | | |
322 VGPQOHVLYIL 332

RESULT 14
A$6059
protein-tyrosine-phosphatase (EC 3.1.3.48) PRL-1 - rat
C;Species: Rattus sp. (rat)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 08-Oct-1999
C;Accession: A56059
R;Diamond, R.H.; Cressman, D.E.; Laz, T.M.; Abrams, C.S.; Taub, R.
Mol. Cell. Biol. 14, 3752-3762, 1994
A;Title: PRL-1, a unique nuclear protein tyrosine phosphatase, affects cell growth.
A;Reference number: A56059; MUID:94254833; PMID:8196618
A;Accession: A56059
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-173 <DIA>
A;Cross-references: GB:I27843; NID:G530161; PIDN:AAA41935.1; PID:G530162
C;Keywords: immediate-early protein; nucleus; phosphoric monoester hydrolase; tyrosine-
Query Match 8.9%; Score 121.5; DB 2; Length 173;
Best Local Similarity 27.5%; Pred. No. 0.0011;
Matches 50; Conservative 52; Indels 57; Gaps 11;

QY      32 MGFPARLELCGVNNDDVVRFI-----DSKHNHYKIYNIICARHYDVA 76

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OV 32 MGFFPAERLEGVYRNNIDVVRF-----DSKHKNHYKIYNLCAERHYDTA 76

Job time : 9.19653 secs

[illegible]

RESULT 15

B44390.
protein-tyrosine-phosphatase (EC 3.1.3.48) PEP, nonreceptor type 8 - mouse
N;Alternate names: protein-tyrosine-phosphatase PEP
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence revision 26-May-1994 #text_change 11-Jun-1999
C;Accession: B44390; S71952; S27876
R;Matthews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L.
Mol. Cell. Biol. 12, 2396-2405, 1992
A;Title: Characterization of Hematopoietic intracellular protein tyrosine phosphatases:
& and threonine-rich sequences.
A;Reference number: A44390; MUID:92236615; PMID:1373816
A;Accession: B44390
A;Molecule type: mRNA
A;Residues: 1-802 <MAT>
A;Cross-references: GB:M90388; NID:G200522; PID:AAA39994.1; PID:G200523
R;Cloutier, J.F.; Veillette, A.
EMBO J. 15, 4909-4918, 1996
A;Title: Association of inhibitory tyrosine protein kinase p50(csk) with protein tyrosin
A;Reference number: S71952; MUID:97045099; PMID:8890164
A;Accession: S71952
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Residues: 495-789 <LO>
C;Comment: This protein is found primarily in hematopoietic tissues.
C;Genetics:
A;Gene: 70zpep
C;Complex: physically associates with inhibitory tyrosine protein kinase Csk; interactio
C;Function:
A;Description: probably an effector and/or regulator of tyrosine protein kinase csk in T
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 8; protein-tyrosine-phosph
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
C;F454-278/Domain: protein-tyrosine-phosphatase homology <P>
F;497-802/Region: glutamic acid/proline/serine/threonine-rich
F;613-621/Region: proline-rich
F;688-695/Region: proline-rich
F;227/Active site: Cys (phosphocysteine intermediate) #status predicted
F;233/Binding site: substrate phosphate (Arg) #status predicted

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Query Match      8.8%; Score 120; DB 1; Length 802;
Best Local Similarity 32.5%; Pred. No. 0.0095;
Matches 49; Conservative 16; Mismatches 44; Indels 42; Gaps 10;

Qy 57 KKKHHYKYLNCERHYDHTAKFNCR-----VAQYFFE---DHNPPQ-----LELIKFFCEDL 105
Db 164 KKKSDYKIRTL-----KAKFNNETRIIYQHYKNWPDHVPSSIDPILQILI----- 209

Qy 106 DQW-----LSEDDNHVAATHCKAGKRGTVMICR-----VLLHRGKFLKQAEALDFYGVGR 156
Db 210 --WDMRCYQEDDCVPICHSAGCGRTGV--ICAVDVTWMLLKDGIIIPKNFSVFNLIQEMR 266

Qy 157 TRDKKGVTIPSORRYVYVYVYVYLL---KNHLD 184

Db 267 T--QRPSLVQIQEQVELVYSAVLBELFRHMD 295

```

Search completed: December 10, 2003, 20:34:59

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:28:57 ; Search time 4.31792 Seconds
(without alignments)
2711.873 Million cell updates/sec

Title: US-09-205-658A-309

Perfect score: 1362

Sequence: 1 I I K E I V S N K R Y Q E D G F D L R R E D K F N Y F P P Q L P V C G D 249

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1354	99.4	403	PTEN_HUMAN	O00633 homo sapien
2	1354	99.4	403	PTEN_MOUSE	O08586 mus musculu
3	478	35.1	551	TPTE_HUMAN	P56180 homo sapien
4	328	24.1	1744	TENS_CHICK	O04205 gallus gall
5	286	21.0	1305	GAK_RAT	P97874 rattus norv
6	285	20.9	1311	GAK_HUMAN	O14976 homo sapien
7	265	19.5	910	AUX1_BOVIN	Q27974 bos taurus
8	244	17.9	434	YNM8_YEAST	P53916 saccharomyc
9	187	13.7	264	YLP1_CAEEL	P91301 caenorhabdi
10	144	10.6	537	FLP1_SCHPO	Q09771 schizosacch
11	129	9.5	551	CL14_YEAST	Q00684 saccharomyc
12	120	8.8	802	PTN8_MOUSE	P29352 mus musculu
13	115	8.4	171	YH01_RACVI	P80994 racoon pox
14	110	8.1	171	DUSP_VARV	P33064 variola vir
15	110	8.1	1897	PTPF_HUMAN	P10586 homo sapien
16	109	8.0	171	DUSP_VACCC	P20495 vaccinia vi
17	109	8.0	171	DUSP_VACCV	P07239 vaccinia vi
18	102.5	7.5	807	PTNM_HUMAN	O9v2r2 homo sapien
19	100.5	7.4	829	PTRA_MOUSE	P18052 mus musculu
20	99.5	7.3	796	PTRA_RAT	Q03348 rattus norv
21	98.5	7.2	802	PTRA_HUMAN	P18433 homo sapien
22	96.5	7.1	168	PTP_NPVAC	Q05209 homo sapien
23	96	7.0	178	PTNC_HUMAN	P24656 autographa
24	95.5	7.0	178	DUSP_MXVVL	Q85297 myxoma viru
25	94	6.9	1312	PTPD_HUMAN	P23468 homo sapien
26	94	6.9	2029	LAR_DROME	P16621 drosophila
27	93	6.8	1063	CDCE_CAEEL	P81299 caenorhabdi
28	92.5	6.8	394	DUS4_HUMAN	Q13115 homo sapien
29	92.5	6.8	395	DUS4_RAT	Q62767 rattus norv
30	92.5	6.8	775	PTNC_MOUSE	P35831 mus musculu
31	92	6.8	2200	LAR_CAEEL	Q9bm8 caenorhabdi
32	91.5	6.7	1301	PTP9_DROME	P35832 drosophila
33	90.5	6.6	482	DUS4_HUMAN	Q9y6w6 homo sapien

RESULT 1

ID	PTEN_HUMAN	STANDARD;	PRT;	403 AA.
AC	O00633; O02679;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase PTEN (EC 3.1.3.67) (Mutated in multiple advanced cancers 1).			
GN	PTEN OR MMAC1 OR TEP1.			
OS	Homo sapiens (Human), and			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606, 9615;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND VARIANTS.			
RC	SPECIES=Human, and C.familiaris;			
RX	MEDLINE=97245711; PubMed=9090379;			
RA	Steck P.A., Pershouse W.A., Jasser S.A., Lin H., Yung W.K.A.,			
RA	Ligon A.H., Langford L.A., Baumgard M.F., Hattier T., Davis T.,			
RA	Frye C., Hu R., Swedlund B., Teng D.H.F., Tavtigian S.V.,			
RT	"Identification of a candidate tumour suppressor gene, MMAC1, at			
RL	chromosome 10q23.3 that is mutated in multiple advanced cancers.";			
RL	Nat. Genet. 15:356-363(1997).			
[2]				
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=97228181; PubMed=9072974;			
RA	Li J., Yen C., Liaw D., Podsypanina K., Bose S., Wang S.I., Puc J.,			
RA	Miliaresis C., Rodgers L., McCombie R., Bigner S.H., Giovanella B.C.,			
RA	Ittmann M., Tycko B., Hibshoosh H., Wigler M.H., Parsons R.;			
RT	"PTEN, a putative protein tyrosine phosphatase gene mutated in human			
RL	brain, breast, and prostate cancer.";			
RL	Science 275:1943-1947(1997).			
[3]				
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=97330649; PubMed=9187108;			
RA	Li D.M., Sun H.;			
RT	"TEP1, encoded by a candidate tumor suppressor locus, is a novel			
RT	protein tyrosine phosphatase regulated by transforming growth factor			
RL	beta.";			
RL	Cancer Res. 57:2124-2129(1997).			
[4]				
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RA	Wang S., Li J., Liaw D., Bose S., Podsypanina K., Parsons R.;			
RL	Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.			
[5]				
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RA	Jensen K., de la Bastide M., Parsons R., Parnell L.D., Dedhia N.,			
RA	Gottesman T., Gnoj L., Kaplan N., Lochi M., Johnson A.F., Shohdy N.,			
RA	Haegawa A., Haberman K., Huang E.N., Schutz K., Calma C., Granat S.,			
RA	Wigler M., McCombie W.R.;			

ALIGNMENTS

- RT "Genomic sequence of PTEN/MMAC1.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RA Gray N.E., Stewart L.M.D., Hamilton J.A., Roberts K.G., Watson G.,
RA Snary D.;
RT "Genomic sequence of chromosome 10q23.3 containing exons 6, 7, 8 and 9
of the PTEN gene.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RA Tissue=lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Ioshyluk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP CHARACTERIZATION.
RC SPECIES=Human;
RX MEDLINE=97404346; PubMed=9256433;
RA Myers M.P., Stolarov J.P., Eng C., Li J., Wang S.I., Wigler M.H.,
RA Parsons R., Tonks N.K.;
RT "p-TEN, the tumor suppressor from human chromosome 10q23, is a dual-
specificity phosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9052-9057(1997).
RN [9]
RP FUNCTION.
RC SPECIES=Human;
RX MEDLINE=98256248; PubMed=9593664;
RA Maehama T., Dixon J.E.;
RT "The tumor suppressor, PTEN/MMAC1, dephosphorylates the lipid second
messenger, phosphatidylinositol 3',4',5'-trisphosphate.";
RL J. Biol. Chem. 273:13375-13378(1998).
RN [10]
RP PHOSPHORYLATION OF THR-366; SER-370 AND SER-385.
RC SPECIES=Human;
RX MEDLINE=22237351; PubMed=12297295;
RA Miller S., Lou D., Seldin D., Lane W., Neel B.;
RT "Direct identification of PTEN phosphorylation sites.";
RL FEBS Lett. 528:145-145(2002).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.10 ANGSTROMS) OF 7-353.
RC SPECIES=Human;
RX MEDLINE=20021619; PubMed=10555148;
RA Lee J.-O., Yang H., Georgescu M.-M., Di Cristofano A., Maehama T.,
RA Shi Y., Dixon J.E., Pandolfi P., Pavlath N.P.;
RT "Crystal structure of the PTEN tumor suppressor: implications for its
phosphoinositide phosphatase activity and membrane association.";
RL Cell 99:323-334(1999).
RN [12]
RP VARIANT CD ASN-137 INS.
RC SPECIES=Human;
RX MEDLINE=98007985; PubMed=9345101;
RA Tsou H.C., Teng D.H.-F., Ping X.L., Brancolini V., Davis T., Hu R.,
RA Xie X.X., Gruener A.C., Schragger C.A., Cristiano A.M., Eng C.,
RA Steck P., Ott J., Tavtigian S.V., Peacocke M.;
RT "The role of MMAC1 mutations in early-onset breast cancer: causative
in association with Cowden syndrome and excluded in BRCA1-negative
cases.";
RL Am. J. Hum. Genet. 61:1036-1043(1997).
RN [13]
RP VARIANTS CD GLU-343 AND LEU-347.
RC SPECIES=Human;
RX MEDLINE=98153621; PubMed=9399897;
RA Lynch E.D., Ostermeyer E.A., Lee M.K., Arena J.F., Ji H., Dann J.,
RA Swisshelm K., Suchard D., Macleod P.M., Kvinnelsland S., Gjertsen B.T.,
RA Heimdal K., Lubs H., Moeller P., King M.-C.;
RT "Inherited mutations in PTEN that are associated with breast cancer,
Cowden disease, and juvenile polyposis.";
RL Am. J. Hum. Genet. 61:1254-1260(1997).
RN [14]
RP VARIANTS CD ARG-123 AND ARG-124.
RC SPECIES=Human;
RX MEDLINE=97402224; PubMed=9259288;
RA Neelen M.R., van Staveren W.C.G., Peeters E.A.J., Ben Hassel M.,
RA Gorlin R.J., Hamm H., Lindboe C.F., Fryns J.-P., Sijmons R.H.,
RA Woods D.G., Mariman E.C.M., Padberg G.W., Kremer H.;
RT "Germline mutations in the PTEN/MMAC1 gene in patients with Cowden
disease.";
RL Hum. Mol. Genet. 6:1383-1387(1997).
RN [15]
RP VARIANT CD GLU-129.
RC SPECIES=Human;
RX MEDLINE=97285123; PubMed=9140396;
RA Liaw D., Marsh D.J., Li J., Dahia P.L.M., Wang S.I., Zheng Z.,
RA Rose S., Call K.M., Tsou H.C., Peacocke M., Eng C., Parsons R.;
RT "Germline mutations of the PTEN gene in Cowden disease, an inherited
breast and thyroid cancer syndrome.";
RL Nat. Genet. 16:64-67(1997).
RN [16]
RP VARIANT B2S ARG-170.
RC SPECIES=Human;
RX MEDLINE=9738233; PubMed=9241266;
RA Marsh D.J., Dahia P.L.M., Zheng Z., Liaw D., Parsons R., Gorlin R.J.,
RA Eng C.;
RT "Germline mutations in PTEN are present in Bannayan-Zonana syndrome.";
RL Nat. Genet. 16:333-334(1997).
RN [17]
RP VARIANT CD GLU-289.
RC SPECIES=Human;
RX MEDLINE=99014194; PubMed=9797362;
RA Chi S.-G., Kim H.-J., Park B.-J., Min H.-J., Park J.-H., Kim Y.-W.,
RA Dong S.-H., Kim B.-H., Lee J.-I., Chang Y.-W., Chang R., Kim W.-K.,
RA Yang M.-H.;
RT "Mutational abrogation of the PTEN/MMAC1 gene in gastrointestinal
polyps in patients with Cowden disease.";
RL Gastroenterology 115:1084-1089(1998).
RN [18]
RP VARIANTS CD HIS-68 AND PRO-112.
RC SPECIES=Human;
RX MEDLINE=98260873; PubMed=9600246;
RA Tsou H.C., Ping X.L., Xie X.X., Gruener A.C., Zhang H., Nini R.,
RA Swisshelm K., Sybert V., Diamond T.M., Sutphen R., Peacocke M.;
RT "The genetic basis of Cowden's syndrome: three novel mutations in
PTEN/MMAC1/TP53.";
RL Hum. Genet. 102:467-473(1998).
RN [19]
RP VARIANTS CD AND B2S.
RC SPECIES=Human;
RX MEDLINE=98133933; PubMed=9467011;
RA Marsh D.J., Coulon V., Lunetta K.L., Rocca-Serra P., Dahia P.L.M.,
RA Zheng Z., Liaw D., Caron S., Duboue B., Lin A.Y., Richardson A.-L.,
RA Bonnetblanc J.-M., Bressieux J.-M., Cabaret-Moreau A., Chompert A.,
RA Demange L., Feles R.A., Yahanda A.M., Fearon E.R., Fricker J.-P.,
RA Gorlin R.J., Hodgson S.V., Huson S., Lacombe D., Leprat F., Odent S.,
RA Toulouse C., Olopade O.I., Sobol H., Tishler S., Woods C.G.,
RA Robinson B.G., Weber H.C., Parsons R., Peacocke M., Longy M., Eng C.;

Query Match 99.4%; Score 1354; DB 1; Length 403;
Best Local Similarity 99.6%; Pred. No. 6.9e-121;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H K N 60
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V I Y S N S G T R R E D K E N Y E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V I Y S N S G T R R E D K E N Y E F 243

QY 241 P Q P L P V C G D 249
DB 244 P Q P L P V C G D 252

RESULT 2

ID PTEN MOUSE
AC O08586;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase PTEN
DE (EC 3.1.3.67) (Mutated in multiple advanced cancers 1).
GN PTEN OR MMAC1
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97245711; PubMed=9090379;
RA Steck P.A., Pershouse M.A., Jasser S.A., Lin H., Yung W.K.A.,
RA Ligon A.H., Langford L.A., Baumgard M.L., Hattig T., Davis T.,
RA Frye C., Hu R., Swedlund B., Teng D.H.F., Tavtigian S.V.;
RT "Identification of a candidate tumour suppressor gene, MMAC1, at
chromosome 10q23.3 that is mutated in multiple advanced cancers.";
RL Nat. Genet. 15:356-363(1997).
CC -!- FUNCTION: Potential tumor suppressor. Acts as a phosphoinositide
CC 3-phosphatase by regulating PtdIns(3,4,5)P3 levels.
CC -!- CATALYTIC ACTIVITY: Phosphatidylinositol-3,4,5-trisphosphate +
CC H(2)O = phosphatidyl inositol-4,5-bisphosphate + phosphate.
CC -!- COFACTOR: Magnesium.
CC -!- PTM: Phosphorylation results in an inhibited activity towards
CC PI3 (By similarity).
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -!- SIMILARITY: Contains 1 tensin domain.
CC -----
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CC -----
DB EMBL; U92437; AAC53118.1; -.
DB MGD; MGI:109583; Pten.
DR GO; GO:0016506; F:apoptosis activator activity; IMP.
DR GO; GO:0016314; F:phosphatidylinositol-3,4,5-trisphosphate 3-...; IDA.
DR GO; GO:0016477; P:cell migration; IMP.

DR GO; GO:0007417; P:central nervous system development; IMP.
DR GO; GO:0006917; P:induction of apoptosis; IMP.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE 2; 1.
KW Hydrolase; Anti-oncogene; Phosphorylation.
FT DOMAIN 22 303
FT ACT_SITE 124 124
FT MOD_RES 366 366
FT MOD_RES 370 370
FT MOD_RES 385 385
SQ SEQUENCE 403 AA; 47152 MW; 75F97C3DD6843BA9 CRC64;

Query Match 99.4%; Score 1354; DB 1; Length 403;
Best Local Similarity 99.6%; Pred. No. 6.9e-121;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H K N 60
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H K N 63

QY 61 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
DB 64 H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123

QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y V Y Y S Y L L K 180
DB 124 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y V Y Y S Y L L K 183

QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V I Y S N S G T R R E D K E N Y E F 240
DB 184 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C O L K V I Y S N S G T R R E D K E N Y E F 243

QY 241 P Q P L P V C G D 249
DB 244 P Q P L P V C G D 252

RESULT 3

ID TPTE HUMAN
AC P56180;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Putative protein-tyrosine phosphatase TPTE (EC 3.1.3.48).
GN TPTE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20065863; PubMed=10598804;
RA Chen H., Rossier C., Morris M.A., Scott H.S., Gos A., Bairoch A.,
RA Antonarakis S.E.;
RT "A testis-specific gene, TPTE, encodes a putative transmembrane
RT tyrosine phosphatase and maps to the pericentromeric region of human
RT chromosomes 21 and 13, and to chromosomes 15, 22, and Y.";
RL Hum. Genet. 105:399-409(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyma S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek K., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,

MEDLINE=97446136; PubMed=9299234;
Kimura S.H., Tsuruga H., Yabuta N., Endo Y., Nojima H.;
"Structure, expression, and chromosomal localization of human GAK.";
Genomics 44:179-187(1997).
[2]
SEQUENCE OF 981-1311 FROM N.A.
TISSUE=Placenta;
MEDLINE=23389257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Locoallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield J.S.N., Krzyzanski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
FUNCTION, AND SUBCELLULAR LOCATION.
MEDLINE=20092914; PubMed=10625686;
Greener T., Zhao X., Nojima H., Eisenberg E., Greene L.E.;
"Role of cyclin G-associated kinase in uncoating clathrin-coated
vesicles from non-neuronal cells";
J. Biol. Chem. 275:1365-1370(2000).
-!- FUNCTION: Associates with cyclin G and CDK5. Seems to act as an
auxilin homolog that is involved in the uncoating of clathrin-
coated vesicles by Hsc70 in non-neuronal cells. Expression
oscillates slightly during the cell cycle, peaking at G1.
-!- SUBCELLULAR LOCATION: Localizes to the perinuclear area and to the
trans-Golgi network. Also seen on the plasma membrane, probably at
focal adhesions.
-!- TISSUE SPECIFICITY: Ubiquitous. Highest in testis.
-!- SIMILARITY: BELONGS TO THE SRP/THR FAMILY OF PROTEIN KINASES.
-!- SIMILARITY: Contains 1 tensin domain.
-!- SIMILARITY: Contains 1 J domain.

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EMBL; D88435; BAA22623.1; --
EMBL; BC000815; AAH00815.1; --
EMBL; BC008658; AAH08658.1; --
Genew; HGNC:4113; GAK.
MIM; 602052; --
GO; GO:0004674; P:protein serine/threonine kinase activity; TAS.
GO; GO:0000074; P:regulation of cell cycle; TAS.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
PROSITE; PS00111; PROTEIN KINASE DOW; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS00636; DnaJ 1; FALSE NEG.

```
DR PROSITE; PS0076; DNAJ_2; 1.  
KW transferase; Serine/threonine-protein kinase; ATP-binding;  
KW Nuclear protein; Endoplasmic reticulum; Cell cycle.  
FT DOMAIN 40 314 PROTEIN KINASE.  
FT ACT SITE 173 BY SIMILARITY.  
FT DOMAIN 347 350 POLY-PRO.  
FT DOMAIN 407 691 TENSIN.  
FT DOMAIN 1247 1311 J-DOMAIN.  
FT CONFLICT 1113 1113 P -> A (in ref. 1).  
SQ SEQUENCE 1311 AA; 143190 MW; OACE45DF57A5F981 CRC64;  
  
Query Match      20.98; Score 285; DB 1; Length 1311;  
Best Local Similarity 29.4%; Pred. No. 7e-19;  
Matches 73; Conservative 47; Mismatches 96; Indels 32; Gaps 10  
  
QY 19 DLDLTITYPNIIAMGPPAEERLEGVYRNNDIVVRFLDSKHKHNYKIYNLCAERHYDTAKF 78  
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
DB 407 DLDISITSIAVMSPFAEGVESALKNNIEDVRLFLSKPGHVAVYNL-SPRTYRPSRF 465  
  
QY 79 NCRVAQYPFDHNPPQLLEIKPFCEDDDLWSEDDNHAAIHCAGKGRTGMICAYILLH 138  
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
DB 466 HNRVSSEGGAARRAPHLHTLYNICRNHMWLQRDQHKNVCVVCHMDGRAASAVAVCSPLCF 525  
  
QY 139 RGFKLAQEALDPYGEVRTDKGVITPSSRRYYVYSLLKKHWLDLRPVA-----LLFH 193  
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
DB 526 CRLFSTAEAAVMYFS--MKRCPPGIW-PSHKRVIYMCDMVAE---EPITPHSKPILV 578  
  
QY 194 KMWFETIPMS--GGTCNPQVFVCOLKV--KLYSSNGPTFRREDKFNYPE-----FP 241  
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
DB 579 AVVTVPVLPSKORSGRCP---FCEVVGDERVAST----SQDYKMRFKIEDGKAVIP 631  
  
QY 242 QPLPVCGD 249  
   :|||:  
DB 632 LGVTVOGD 639  
  
RESULT 7  
AUXI_BOVIN STANDARD; PRT; 910 AA.  
AC Q2797a;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Auxilin.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=95220355; PubMed=7705342;  
RA Schroeder S., Morris S.A., Knorr R., Plesseman U., Weber K.,  
  Vinh N.G., Ungewickell E.;  
RT "Primary structure of the neuronal clathrin-associated protein  
  auxilin and its expression in bacteria.";  
RL Eur. J. Biochem. 228:297-304(1995).  
CC -/- FUNCTION: BINDS CLATHRIN HEAVY CHAIN AND PROMOTES ITS ASSEMBLY  
    INTO REGULAR CAGES.  
CC CC  
CC -/- TISSUE SPECIFICITY: BRAIN.  
CC -/- PTM: THE N-TERMINUS IS BLOCKED.  
CC -/- PTM: TARGET FOR COAT-ASSOCIATED CASEIN KINASE II IN VITRO.  
CC -/- SIMILARITY: Contains 1 tensin domain.  
CC -/- SIMILARITY: Contains 1 J domain.  
CC -----  
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CC EMBL; U09237; AA79037.1; -.
CC PIR; S68983; S68983.
CC InterPro; IPR001623; DnaJ_N.
CC Pfam; PF00226; TYR_phosphatase.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; UNKNOWN 1.
CC PROSITE; PS00506; TYR_PHOSPHATASE_2; UNKNOWN 1.
CC PROSITE; PS06336; DnaJ_1; FALSE_NEG.
CC PROSITE; PS0076; DnaJ_2; 1.
CC SH3-binding; Repeat; Phosphorylation.
KW DOMAIN 33 44
FT REPEAT 33 36
FT REPEAT 37 40
FT REPEAT 41 44
FT DOMAIN 60 344
FT SITE 406 414 SH3-BINDING (POTENTIAL).
FT DOMAIN 463 757 PRO-RICH.
FT DOMAIN 526 529 POLY-GLY.
FT DOMAIN 846 910 J-DOMAIN.
SQ SEQUENCE 910 AA; 99512 MW; BC156DC1CF3487FD CRC64;

Query Match 19.5%; Score 265; DB 1; Length 910;
Best Local Similarity 28.8%; Pred. No. 3.5e-17;
Matches 66; Conservative 46; Mismatches 99; Indels 18; Gaps 7;

QY 1 I I K E I V S R N K R Y Q E D G F D L D L T Y P N I I A M G F P A E R L E G Y V R N N I D D V V R F L D S K H N 60
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
49 V I Q S V T S Y T K G - - - - - D L D F T Y T S R I I V M S P F L D S V D I G F R N Q V D D I R S F L D S R H L D 101

QY 61 H Y K I Y N L C A E R H Y D T A K N C R V A Q Y P F E D H N P P Q L E L I K P C E D L D W L S E D D N H V A I H 120
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
102 H Y T V N L - S P K S Y R T A K F H S R V S E C S W P I R Q A P S L H N L F A V C R N N Y N W L L Q N P K N V C V V H 160

QY 121 C K A G R G T G V M I C A V L L H R G F L K A Q E A L D F Y G E V T R D K K G V T I - P S O R R V V Y Y S Y L L 179
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
161 C L D G R A A S I L V G A M F I C N L Y S T G P A V - - - - - R L L Y A K R P G I G U S P H R R Y L G Y M C D L L 216

QY 180 K N H L D Y R P - V A L L F H K M F E T I M F S - G G T C N P Q F V V C Q L K V I Y S S 224
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
217 A D K - P Y R H F R E P L T I K S I T V S P V P F N K O R G C R Y C D V L I G E T K I Y T T 264

RESULT 8
YNM8 YEAST
ID YNM8 YEAST STANDARD; PRT; 434 AA.
AC P53916;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical 50.2 kDa protein in CP1-SPC98 intergenic region.
GN YNL128W OR N1220 OR N1872.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=96109932; PubMed=8619318;
RA Mallet L., Bussereau F., Jacquet M.;
RT "A 43.5 kDa segment of yeast chromosome XIV, which contains MPA2,
RT MEP2, CAP/SRV2, NAM9, FKBP1/PP1/RBP1, MOM22 and CP1, predicts an
RT adenosine deaminase gene and 14 new open reading frames.",
RL Yeast 11:1195-1209(1995).
CC -!- SIMILARITY: SOME, TO PROTEIN-TYROSINE PHOSPHATASES.
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-----
CC EMBL; U88173; AA021381.1; -.
CC PIR; T25762; T25762.
CC WormPep; F46F11.3; CE10600.
KW Hypothetical protein.
FT DOMAIN 31 264
SQ SEQUENCE 264 AA; 30300 MW; 3DF3698F292BC5E5 CRC64;

Query Match 13.7%; Score 187; DB 1; Length 264;
Best Local Similarity 21.9%; Pred. No. 1.9e-10;
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-----
DR EMBL; Z46843; CAA86897.1; -.
DR EMBL; Z71404; CAA96010.1; -.
DR PIR; S55155; S55155.
DR SGD; S0005072; TEPI.
DR GO; GO:0004437; F:inositol/phosphatidylinositol phosphatase a...; IDA.
DR GO; GO:0007152; P:spore wall assembly (sensu Saccharomycetes); IMP.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00506; TYR_PHOSPHATASE_2; 1.
KW Hypothetical protein; Hydrolase.
SQ SEQUENCE 434 AA; 50152 MW; E56739475D1FA898 CRC64;

Query Match 17.9%; Score 244; DB 1; Length 434;
Best Local Similarity 27.6%; Pred. No. 1.4e-15;
Matches 66; Conservative 41; Mismatches 64; Indels 68; Gaps 9;

QY 1 I I K E I V S R N K R Y Q E D G F D L D L T Y P N I I A M G F P A E R L E G Y V R N N I D D V V R F L D S K H N 58
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
22 L M K K I L S L P M K K T K N D I G L R D I S Y I L V N L I V C S Y P V N T Y P K L L Y R N S L D D L I L F L T V Y H 81

QY 59 - K N H Y K I Y N L C A E R H Y D T A K E N - - - - - C R V A Q Y P F E - - - - - 88
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
82 G K G N F R I P N F R G E K E D S Y K D N D L I G I A A K P E S K D F E I Q E L R S T L I N D K G I P I S I D L E T 141

QY 89 - - - - - D H N P P Q L E L I K P C E D L D W L S E D D N H V A I H C K A G R G T G 129
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
142 R T L V E E T N N V I C E R I G W L D H F P P P F E L L E I V D G I E N Y L S V S K R V A V L H C R M G K G R S G 201

QY 130 V M I C A Y L L H R G F L K A Q E A L D F Y G E V R - - - - - T R D K - - - - - K G V T I P S O R R V V Y Y S Y L L 179
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
202 M I T V A Y L M - - - - - K Y L Q C P - - - - - L G E A R L I F M Q A R F K Y G M T G N G V T I P S O L R Y L R Y H E F F I 252

RESULT 9
YLPK_CABEL
ID YLPK_CABEL STANDARD; PRT; 264 AA.
AC P91301;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 30.3 kDa protein F46F11.3 in chromosome I.
GN F46F11.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Gattung S.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 tensin domain.
-----
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-----
DR EMBL; U88173; AA021381.1; -.
DR PIR; T25762; T25762.
DR WormPep; F46F11.3; CE10600.
KW Hypothetical protein.
FT DOMAIN 31 264
SQ SEQUENCE 264 AA; 30300 MW; 3DF3698F292BC5E5 CRC64;

Query Match 13.7%; Score 187; DB 1; Length 264;
Best Local Similarity 21.9%; Pred. No. 1.9e-10;
-----
```

Matches	56; Conservative	56; Mismatches	120; Indels	24; Gaps	7
1	IIKEIVSNKRKYQBDGFDLDITYIPNIIANGFPAERLEGVYRNINDDVVRFLDSKHQ	60			
15	LVEKLRKKQKMDRKEGVQVE--YITSLRILVLSCTSETSERKFVESLLKASQIQAHNK	72			
61	HVKIYNLCAERHYDTAKNCRVAQYFPEDHNPQLELIKPFCEDDLDWLSDDNHNVAIH	120			
73	HIRVNVNSGRRHDISSSLDAIEFGPSE--TAPSLKJCTICKNIDQWMLHPLNIAVIF	130			
121	CKAGKRTGVMI CAYLLHRGKFLKAQEAALDFGEVTRDK----EGVTIPSORRYVYYS	176			
131	CKGGLERCAIVNAFMRFNAISATSDSVDDRESMQRFSERFGLGDPG--PSYKRYLGVFS	188			
177	YLLKNHLDYRPVALLFHQNM---FETIPMFSGGTCNPQPVWCOLKVIYSSNSGPTRED	233			
189	SLLSGRISVNSDPLYLHNILITFFEPINF-----LKTYERLVPVTSQKVALNKSS	240			
234	KFNYPEFPQPLFVPCGD	249			
241	K---FEMDGLSKLRGD	253			

RESULT 10

CD	FLP1_SCHPO	STANDARD;	PRT;	537 AA.
C	Q9P7H1;			
I	28-FEB-2003	(Rel. 41, Created)		
T	28-FEB-2003	(Rel. 41, Last sequence update)		
T	28-FEB-2003	(Rel. 41, Last annotation update)		
E	Protein-tyrosine phosphatase CDC14 homolog (EC 3.1.3.48) (CDC			
E	fourteen-like phosphatase 1).			
N	FLP1 OR SPAC1782.09C.			
S	Schizosaccharomyces pombe (Fission yeast).			
C	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
C	Schizosaccharomycetales; Schizosaccharomycetaceae;			
C	Schizosaccharomycetes.			
X	NCBI_TaxID=4896;			
N	[1]			
N	SEQUENCE FROM N.A.			
C	STRAIN=972;			
C	MEDLINE=21848401; PubMed=11859360;			
X	Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,			
A	Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,			
A	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,			
A	Collins M., Connor A., Cronin A., Davis P., Fellwell T., Fraser A.,			
A	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,			
A	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,			
A	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,			
A	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeell C.,			
A	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,			
A	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,			
A	Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,			
A	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,			
A	Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,			
A	Welljens I., Vanstreels E., Rigger M., Schaefer M., Mueller-Auer S.,			
A	Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,			
A	Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,			
A	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,			
A	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,			
A	Gallibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,			
A	Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,			
A	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,			
A	Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,			
A	Cherkovski L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,			
A	Shaputski G.V., Ussery D., Barrell B.G., Nurse P.;			
T	"The genome sequence of Schizosaccharomyces pombe.";			
L	Nature 415:871-880(2002).			
L	[2]			
N	FUNCTION, SUBCELLULAR LOCATION, AND PHOSPHORYLATION.			
X	MEDLINE=21539578; PubMed=11683392;			
X	Cueille N., Salimova E., Esteban V., Blanco M., Moreno S., Bueno A.,			
X	Simanis V.			

```

"Flp1, a fission yeast orthologue of the s. cerevisiae CDC14 gene, is
not required for cyclin degradation or rumpl stabilisation at the end
of mitosis.";
J. Cell Sci. 114:2649-2664(2001).
CC -!- FUNCTION: Has a role in regulating entry into mitosis and promotes
CC septum signaling.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolus until mitosis and the
CC spindle pole body through to late anaphase.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. CDC14 SUBFAMILY.
-----
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-----
EMBL; AL158056; CAB76271.1; -.
DR PIR; T50099; T50099.
DR HSP; P29350; 1GZW.
DR GeneDB; SPombe; SPAC1782.09c; -.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSEC; 1.
DR PRINTS; PR00700; PRTYPHPHTASE.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase; Cell cycle; Mitosis; Septation; Nuclear protein;
KW Phosphorylation.
FT ACT_SITE 286
FT SEQUENCE 537 AA; 60253 MW; F5E50A8C0924C7EA CRC64;
-----
Query Match 10.6%; Score 144; DB 1; Length 537;
Best Local Similarity 24.6%; Pred. No. 5.4e-06;
Matches 57; Conservative 32; Mismatches 67; Indels 76; Gaps 11;

QY 2 IKEIVSRNRRYQ--BDGFDLDTYIYPNIIAMGFPAER-----LE 40
| | | | | | | | | | | | | | | | | | | | | | | | | |
| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 164 IRNIDVHDYETVERVENG---DFNWI5PKFIAP5PIQAGWNHASTRPKKLPQPFIVLD 220
| | | | | | | | | | | | | | | | | | | | | | | | | |
QY 41 GVYRNNDIVVRF-----LDSKHKHXYKIYNLCAEHYDTAKENCVAQYPFE 88
| | | | | | | | | | | | | | | | | | | | | | | | | |
| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 221 YFVANKVKILVRUNGPLYDKTFFENVGIHKEMY-----FE 256
| | | | | | | | | | | | | | | | | | | | | | | | | |
QY 89 DHNPPOLEILKPCEDLDOWLSDDNHVAIHCAGKGRGTVMICAYLLHRGKFLKAQEA 148
| | | | | | | | | | | | | | | | | | | | | | | | | |
| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 257 DGVTPSLSVKEFI-DLTEVEEDG--VTAVHCAGLGRGTGLIGAYLYIKHCF-TANEV 312
| | | | | | | | | | | | | | | | | | | | | | | | | |
QY 149 LDFYGEVTRTDKGVTPISQRRYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 200
| : | : | : | : | : | : | : | : | : | : | : | : | : |
| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 313 IAVWRIMR---PGMVVGPOHMLHI-----NOVHFR--AYFEKAMGRAI 352
| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
CC14 YEAST
ID CC14 YEAST STANDARD; PRT; 551 AA.
AC Q00684;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable protein-tyrosine phosphatase CDC14 (EC 3.1.3.48).
GN CDC14 OR YFR028C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.

```



```
Db 210 --WDMRCYQEDDCVPCICHSAGCGRTGV-ICAVDTYTWLLKDGIIIPKNFSVFNLIQEMR 266
QY 157 TRDKGVITPSORRYYVYSYLL---KNHLD 184
Db 267 T--QRPSLVQTEQVELVYSAVLEFLFKRHMD 295

RESULT 13
VH01 RACVI
ID VH01 RACVI STANDARD; PRT; 171 AA.
AC P80994;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dual specificity protein phosphatase (EC 3.1.3.48) (EC 3.1.3.16) (Late
protein H1).
GN VH1.
OS Raccoon poxvirus (RCN).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10256;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93248221; PubMed=8387208;
RA Hakes D.J., Martell K.J., Zhao W.G., Massung R.F., Esposito J.J.,
RA Dixon J.E.;
RT "A protein phosphatase related to the vaccinia virus VHL is encoded
in the genomes of several orthopoxviruses and a baculovirus.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4017-4021(1993).
CC -!- FUNCTION: Shows activity toward tyrosine-protein phosphate as well
as with serine-protein phosphate.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -----
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CC -----
CC EMBL; L13165; -; NOT ANNOTATED_CDS.
CC PIR; B47452; B47452.
CC InterPro; IPR000340; DS_phosphatase.
CC InterPro; IPR000387; TYR_phosphatase.
CC Pfam; PF00782; DSPC; 1.
CC SMART; SM00195; DSPC; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
CC Hydrolase; Late protein.
FT ACT SITE 110 110 BY SIMILARITY.
SQ SEQUENCE 171 AA; 19741 MW; 503416F4988B3E81 CRC64;

Query Match 8.4%; Score 115; DB 1; Length 171;
Best Local Similarity 28.3%; Pred. No. 0.00073;
Matches 41; Conservative 24; Mismatches 68; Indels 12; Gaps 7;

QY 42 VYRNIDVVRFLDSKHKHXYKTYNLCARHYDTAKFNCRCVQYPPEDHNPQLEIKPF 101
Db 34 VYLGNYKNAMAPSPSEVKFY-ILNLTMDK-VSFTNSNINIHPVMDTSTDISI---Y 88

QY 102 CEDLDOWLSGDD--NHVAIAHCKAGKGRGTGMICAYLLHRGKFLKAQELDF-YGEVRR 158
Db 89 FDDITAFLEKCDORNEPVLVHCAGVNRSGAMILAYLMSKNK--ESSPMLYFLYVHNR 146

QY 159 DKKGVTI--PSQRRYYVYSYLLKN 181
Db 147 DLRGAFVENPFSKRIIEKYVIDKN 171
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RESULT 14
DUSP_VARV
ID DUSP_VARV STANDARD; PRT; 171 AA.
AC P33064;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dual specificity protein phosphatase (EC 3.1.3.48) (EC 3.1.3.16) (Late
protein H1).
GN H1L OR ILL.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=India-1967 / Isolate Ind3;
RX MEDLINE=93190624; PubMed=8383392;
RA Shchelkunov S.N., Blinov V.M., Tormenin A.V., Marennikova S.S.,
RA Kolykhalov A.A., Frolov I.V., Chizhikov V.E., Gytarov V.V.,
RA Gashikov P.V., Belanov E.F., Belavin P.A., Resenchuk S.M.,
RA Andzhaparidze O.G., Sandakhchiev L.S.;
RT "Nucleotide sequence analysis of variola virus HindIII M, L, I genome
fragments.";
RL Virus Res. 27:25-35(1993).
RN [2]
RP COMPLETE GENOME.
RX STRAIN=India-1967 / Isolate Ind3;
RX MEDLINE=93202281; PubMed=8384129;
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Bangladesh-1975;
RX MEDLINE=94088747; PubMed=8264798;
RA Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
RA Venter C.J.;
RT "Potential virulence determinants in terminal regions of variola
smallpox virus genome.";
RL Nature 366:748-751(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=Garcia-1966;
RA Shchelkunov S.N., Balkin I.V., Tormenin A.V., Resenchuk S.M.,
RA Blinov V.M., Sandakhchiev L.S.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Shows activity toward tyrosine-protein phosphate as well
as with serine-protein phosphate.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -----
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CC -----
CC EMBL; X671119; CAA47583.1; -
CC EMBL; S55844; AAB24680.1; -
CC EMBL; X69198; CAA49025.1; -
CC EMBL; U22579; AAA60832.1; -
CC EMBL; X76264; CAA53838.1; -
CC PIR; B72161; B72161.
CC PIR; I36845; I36845.
```


CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 8 fibronectin type III domains.
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC
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CC
CC EMBL; Y00815; CAA68754.1; -
CC PIR; S03841; TDHULK.
CC PDB; 1LAR; 25-APR-00.
CC Genew; HGNC:9670; PTPRF.
CC MIM; 179590;
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005001; P: transmembrane receptor protein tyrosine pho. .; TAS.
CC GO; GO:0007155; P: cell adhesion; TAS.
CC GO; GO:0007185; P: transmembrane receptor protein tyrosine pho. .; TAS.
CC InterPro; IPR003961; FN III, subd.
CC InterPro; IPR003962; FN III, subd.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003598; IG c2.
CC InterPro; IPR003006; IG MHC.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00041; fn3; 7.
CC Pfam; PF00047; ig; 3.
CC Pfam; PF00102; Y_phosphatase; 2.
CC PRINTS; PR00014; ENTYPRIII.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00060; FN3; 4.
CC SMART; SM00408; IGC2; 3.
CC SMART; SM00194; PTPC; 2.
CC PROSITE; PS50835; IG LIKE; 3.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
CC PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
CC Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
CC Cell adhesion; Immunoglobulin domain; Repeat; 3D-structure.
CC SIGNAL 1 16
CC CHAIN 17 1897
CC DOMAIN 17 1250
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 1251 1274
CC POTENTIAL.
CC DOMAIN 1275 1897
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 23 1137
CC IG-LIKE C2-TYPE 1.
CC DOMAIN 125 214
CC IG-LIKE C2-TYPE 2.
CC DOMAIN 222 304
CC IG-LIKE C2-TYPE 3.
CC DOMAIN 1360 1606
CC PROTEIN-TYROSINE PHOSPHATASE 1.
CC DOMAIN 1649 1897
CC PROTEIN-TYROSINE PHOSPHATASE 2.
CC ACT SITE 1538 1538
CC BY SIMILARITY.
CC ACT SITE 1829 1829
CC BY SIMILARITY.
CC FT CARBOHYD 107 107
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 240 240
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 285 285
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 711 711
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 956 956
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT MUTAGEN 1538 1538
CC C->S: LOSS OF ACTIVITY.
CC SEQUENCE 1897 AA; 211844 MW; 439850F1D5C031FF CRC64;

CC Query Match 8.1%; Score 110; DB 1; Length 1897;
CC Best Local Similarity 23.5%; Pred. No. 0.044;
CC Matches 46; Conservative 30; Mismatches 88; Indels 32; Gaps 9;

CC QY 51 VRFLDKSHKHYKYNLCARHYDTAKFCNCRVAQY-PFEDHNPQ-----LELIKPF 101
CC DB 1467 VTLDTVLELATYVTRTFALHKSQSGSEKRELQFOFMANPDHGVETPTPLAFRRVKA- 1525
CC QY 102 CEDLDQWLSEDDNHVAHHCAGKGRGTGVNICA-YLLHRGKFLKAQBALDFYGEVR-TRD 159

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: December 10, 2003, 20:29:32 ; Search time 14.1874 Seconds
(without alignments)
4529.010 Million cell updates/sec

Title: US-09-205-658A-309
Perfect score: 1362
Sequence: 1 IIKEIVSNKRYQEDGFDL.....REDKFNFFPQLPVCGD 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1348	99.0	403	11	O54857
2	1308	96.0	403	4	O43460
3	1294	95.0	338	4	O14781
4	1266	93.0	412	13	O90XY3
5	1189	87.3	402	13	O9PUT6
6	1136	83.4	369	4	O8IVA5
7	695	51.0	280	11	O8BSR7
8	641.5	47.1	418	5	O9Y0B6
9	641.5	47.1	506	5	O9U470
10	641.5	47.1	509	5	O9V3L4
11	641.5	47.1	511	5	O9Y0B5
12	641.5	47.1	514	5	O9V413
13	603.5	44.3	515	5	O8T658
14	603.5	44.3	533	5	O8T9S7
15	517	38.0	611	10	O9LT75
16	517	38.0	611	10	O8GZT8

17	516	37.9	326	4	O8WNL4
18	514.5	37.8	628	10	O9SN07
19	514.5	37.8	632	10	O8HI06
20	511	37.5	445	4	O8WNL5
21	494	36.3	591	11	O91X01
22	494	36.3	645	11	O91X02
23	494	36.3	664	11	O91X03
24	478	35.1	533	4	O8NCS8
25	476	34.9	412	10	O9FLZ5
26	465	34.1	962	5	O44405
27	350	25.7	1735	4	O9HBL0
28	346	25.4	1715	6	O9GLM4
29	340	25.0	624	11	O8BJA7
30	339.5	24.9	391	4	O8NAD0
31	339.5	24.9	1445	4	O8IZW7
32	309	22.7	348	3	O94526
33	301.5	22.1	1285	4	O9UPS7
34	301.5	22.1	1409	4	O8NFF9
35	301.5	22.1	1419	4	O8NFG0
36	296	21.7	398	4	O8NV48
37	294.5	21.6	1381	11	O8CJ95
38	294.5	21.6	1400	11	O8CGB6
39	282.5	20.7	222	11	O8C6V6
40	271	19.9	913	4	O75061
41	246	18.1	885	11	O8BM74
42	212	15.6	77	4	O9HLM7
43	149	10.9	1165	5	O9VMY8
44	129	9.5	326	3	O05673
45	129	9.5	551	3	O05180

ALIGNMENTS

RESULT 1

O54857 PRELIMINARY; PRT; 403 AA.
ID O54857
AC O54857;
DC 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Protein tyrosine phosphatase and tensin homolog/mutated in multiple
DE advanced cancers protein.
GN PTEN/MMAC1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Roz L., Finocchiaro G.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF017185; AAB96620.1; -
DR InterPro; IPR000387; TYR_PHOSPHATASE.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 403 AA; 47118 MW; 243BFE35FE209FE5 CRC64;

Query Match 99.0%; Score 1348; DB 11; Length 403;
Best Local Similarity 99.2%; Pred. No. 1.3e-124;
Matches 247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY	1	I I K E I V S N K R Y Q E D G F D L T I Y P N I I A M G P P A E R L E G V Y R N I I D V V R F L D S K H K N	60
DB	4	I I K E I V S N K R Y Q E D G F D L T I Y P N I I A M G P P A E R L E G V Y R N I I D V V R F L D S K H K N	63
OY	61	H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P P R E D H N P P O L E L I K P F C E D L D Q M L S E D D N V A A I H	120
DB	64	H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P P R E D H N P P O L E L I K P F C E D L D Q M L S E D D N V A A I H	123
OY	121	C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G V R T R D K R G V T I P S Q R R Y V Y Y Y L L K	180

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Db 124 CKAAGKRTGVMICAYLLHRGKFLKAQALDFYGEVTRDKKGVTPSQRRYVYYSLLK 183
QY 181 NHDYRPVALLFHKKMFETIPMFSGTCNPQFVVCQKVKIYSSNSGPTREDKFNYPFF 240
Db 184 NHDYRPVALLFHKKMFETIPMFSGTCNPQFVVCQKVKIYSSNSGPTREDKLMYFEF 243
QY 241 PQLPVCVD 249
Db 244 PQLPVCVD 252

RESULT: 2
O43460 PRELIMINARY; PRT; 403 AA.
AC O43460;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JAN-2003 (TrEMBLrel. 23, Last annotation update)
DE Phosphatase and tensin homolog 2 (Fragment).
GN PTH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98127441; PubMed=9467947;
RA Kim S.K., Su L.K., Oh Y., Kemp B.L., Hong W.K., Mao L.;
RT "Alterations of PTEN/MMAC1, a candidate tumor suppressor gene, and its
RT homologue, PTH2, in small cell lung cancer cell lines.";
RL Oncogene 16:89-93 (1998).
DR EMBL; AF019083; AAC52017.1; -.
DR Genbank; HGNC:9589; PTENP1.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
FT NON_TER 1
SQ SEQUENCE 403 AA; 47163 MW; BDD42A4D0F26B419 CRC64;

Query Match 96.0%; Score 1308; DB 4; Length 403;
Best Local Similarity 96.8%; Pred. No. 1.1e-120;
Matches 241; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 63
QY 61 H Y K I N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 64 H Y K I H N L C A E R H Y D T A K S N Y R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180
Db 124 C K A G K R T G I M I C A Y L L H R G K F L K A Q E A L D F Y G E V T R D K K G V T I P S Q R R Y V Y Y S Y L L K 183
QY 181 N H D Y R P V A L L F H K M F E T I P M F S G T C N P Q F V V C Q K V K I Y S S N S G P T R E D K F N Y P F F 240
Db 184 N H D Y R P V A L L F H K M F E T I P M F S G T C N P Q F V V C Q K V K I Y S S N S G P T R E D K F M Y P E F 243
QY 241 P Q L P V C G D 249
Db 244 P Q L P V C G D 252

RESULT 3
O14781 PRELIMINARY; PRT; 338 AA.
ID O14781;
AC O14781;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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```
DE Hypothetical protein (Fragment).
GN PTEN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99008335; PubMed=9794233;
RA Forgas E., Biesterveld E.J., Sekido Y., Fong K., Muneer S.,
RA Wistuba I.I., Milchgrub S., Brezinschek R., Virmani A., Gazdar A.F.,
RA Minna J.D.;
RT "Mutation analysis of the PTEN/MMAC1 gene in lung cancer.";
RL Oncogene 17:1557-1565 (1998).
DR EMBL; AF017999; AAB70558.1; -.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hypothetical protein; Hydrolase.
FT NON_TER 1
FT NON_TER 338
SQ SEQUENCE 338 AA; 39899 MW; 63F3F51FBA9FA305 CRC64;

Query Match 95.0%; Score 1294; DB 4; Length 338;
Best Local Similarity 96.0%; Pred. No. 2.2e-119;
Matches 239; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 60
Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H K N 63
QY 61 H Y K I N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 120
Db 64 H Y K I H N L C A E R H Y D T A K S N Y R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A A I H 123
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V T R D K K G V T I P S Q R R Y V Y Y S Y L L K 180
Db 124 C K A G K R T G I M I C A Y L L H R G K F L K A Q E A L D F Y G E V T R D K K G V T I P S Q R R Y V Y Y S Y L L K 183
QY 181 N H D Y R P V A L L F H K M F E T I P M F S G T C N P Q F V V C Q K V K I Y S S N S G P T R E D K F N Y P F F 240
Db 184 N H D Y R P V A L L F H K M F E T I P M F S G T C N P Q F V V C Q K V K I Y S S N S G P T R E D K F M Y P E F 243
QY 241 P Q L P V C G D 249
Db 244 P Q L P V C G D 252

RESULT 4
Q90XY3 PRELIMINARY; PRT; 412 AA.
ID Q90XY3;
AC Q90XY3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PTEN.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21455682; PubMed=11571655;
RA Yu W.P., Pallen C.J., Tay A., Jirik F.R., Brenner S., Tan Y.H.,
RA Venkatesh B.;
RT "Conserved synteny between the Fugu and human PTEN locus and the
RT evolutionary conservation of vertebrate PTEN function.";
RL Oncogene 20:5554-5561 (2001).
DR EMBL; AF325922; AAL08419.1; -.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
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DR PROSITE, PSS0056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 412 AA; 47974 MW; 8ABEBD8B71346CE3 CRC64;

Query Match
Best Local Similarity 93.0%; Score 1266; DB 13; Length 412;
Matches 231; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 I I K E I V S N K R Y Q D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V R F L D S K H K N 60
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 4 I I K E V S N K R Y Q D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V R F L D S K H K N 63
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 H Y K I N L C A E R H Y D T A K N C R V A O Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A I H 120
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 H Y K I N L C A E R H Y D A K N C R V A O Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A I H 123
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 180
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 124 C K A G K R T G V M I C A Y L L H R G K F L D A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 183
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N G S P T R R E D K F N Y P E F 240
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 N Q L E Y K P V A L L F H K M F E T L P M F S G G T C N P Q V V C Q L K V K I Y S S N G S P T R R E D K H M F E F 243
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 241 P Q L P V C G D 249
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 244 P Q L P V C G D 252
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
Q9PUT6 PRELIMINARY; PRT; 402 AA.
ID Q9PUT6
AC Q9PUT6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein/lipid phosphatase Pten.
GN Pten.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesopodactylia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20021619; PubMed=1055148;
RA Lee J.O., Yang H., Georgescu M.M., Di Cristofano A., Maehama T.,
RA Shi Y., Dixon J.E., Pandolfi P., Pavletich N.P.;
RT "Crystal structure of the Pten tumor suppressor: implications for its
RT phosphoinositide phosphatase activity and membrane association.";
RL Cell 99:323-334 (1999).
DR EMBL; AF144732; AAD46165.1;
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 402 AA; 46878 MW; E61315E2DAB0805F CRC64;

Query Match
Best Local Similarity 87.3%; Score 1189; DB 13; Length 402;
Matches 222; Conservative 12; Mismatches 13; Indels 2; Gaps 2;

QY 1 I I K E I V S N K R Y Q D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V R F L D S K H K N 60
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 4 I I K E V S N K R Y Q D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N I D D V R F L D S K H K N 63
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 H Y K I N L C A E R H Y D T A K N C R V A O Y P F E D H N P P Q L E L K P F C E D L D W L S E D D N H V A I H 120
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 H Y K I N L C A E R H Y D T K F S C R V A O Y P F E D H N P P Q L E L K P F C E D L D L S E N E N - V A A I H 122
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K 180
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q V V C Q L K V K I Y S S N G S P T R R E D K F N Y P E F 240
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 N Q L E Y K P V A L L F H K M F E T L P M F S G G T C N P Q V V C Q L K V K I Y S S N G S P T R R E D K H M F E F 243
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 241 P Q L P V C G D 249
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 244 P Q L P V C G D 252
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
Q8IVAS PRELIMINARY; PRT; 369 AA.
ID Q8IVAS
AC Q8IVAS;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to phosphatase and tensin homolog (Mutated in multiple
DE advanced cancers 1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX STRAUSBERG R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038293; AAH38293.1;
SQ SEQUENCE 369 AA; 43133 MW; 8A28D666567CD777 CRC64;

Query Match
Best Local Similarity 83.4%; Score 1136; DB 4; Length 369;
Matches 207; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 32 M G F P A E R L E G Y V R N I D D V R F L D S K H K N H Y K I Y N L C A E R H Y D T A K N C R V A O Y P F E D H N 91
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1 M G F P A E R L E G Y V R N I D D V R F L D S K H K N H Y K I Y N L C A E R H Y D T A K N C R V A O Y P F E D H N 60
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 92 P P Q L E L K P F C E D L D W L S E D D N H V A I H C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F 151
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 P P Q L E L K P F C E D L D W L S E D D N H V A I H C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F 120
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 152 Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q 211
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 Y G E V R T R D K K G V T I P S Q R R V V Y Y S Y L L K N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q 180
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 212 F V C Q L K V K I Y S S N G S P T R R E D K F N Y P F P Q L P V C G 248
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 F V C Q L K V K I Y S S N G S P T R R E D K F N Y P F P Q L P V C G 217
D b : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
Q8BSR7 PRELIMINARY; PRT; 280 AA.
ID Q8BSR7
AC Q8BSR7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phosphatase and tensin homolog (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
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RL Nature 420-563-573(2002).
DR EMBL; AK030750; BAC27118.1; -.
FT NON_TER
SQ SEQUENCE 280 AA; 32522 MW; 7077A05A89ABCF2 CRC64;

Query Match
Best Local Similarity 51.0%; Score 695; DB 11; Length 280;
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 121 CKAGKGRGTGVTICAYLLHRRGKFLKQAEALDFYGEVTRDKKGVITPSQRRYYVYVYLLK 180
Db |||
1 CKAGKGRGTGVTICAYLLHRRGKFLKQAEALDFYGEVTRDKKGVITPSQRRYYVYVYLLK 60

QY 181 NHLDRPVALLPHKMFETIPMFSGTGNPQFVWCQVKIYSSNGTPTREDKKNYFEF 240
Db |||
61 NHLDRPVALLPHKMFETIPMFSGTGNPQFVWCQVKIYSSNGTPTREDKKNYFEF 120

QY 241 POPLPVCGD 249
Db |||
121 POPLPVCGD 129

RESULT 8
QY086 PRELIMINARY; PRT; 418 AA.
ID QY086
AC QY086;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE PTEN1 (EC 3.1.3.48) (CG5671-PC).
DE PTEN OR CG5671.
GN PTEN
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_TaxID=7227;
RP SEQUENCE FROM N.A.
RA Smith A.;
RT "Alternative splicing of the Drosophila PTEN Gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H., Blazek R.G., Champs M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Barzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Dou L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragov V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
SEQUENCE FROM N.A.
RA Flybase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161257; AAD45362.1; -
DR EMBL; AE003628; AAN10730.1; -
DR FlyBase; FBgn0026379; Pten.
DR InterPro; IPR000215; Serpin.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00566; TYR_PHOSPHATASE_2; 1.
DR Hydrolase.
RW SEQUENCE 418 AA; 48066 MW; 89A6C4DDCCDDBA40 CRC64;

Query Match
Best Local Similarity 47.1%; Score 641.5; DB 5; Length 418;
Matches 130; Conservative 41; Mismatches 72; Indels 17; Gaps 5;

QY 1 I I K E I V S R N K R Y Q D G D F D L T I Y P N I A M G P P A - B R L S G V Y R N N D D V R F L D S K H K 59
Db |||
11 V I R N V S K R I R Y K E G Y D L D L T I N D I I A M G V P A P D K L E G L F E R N L E D V F K L L E E N H A 70

QY 60 N H Y K I N I C A E R H Y D T A K F N C R V A Q Y P E D H N P P O L E I I K P C E D D L D S D D N H V A A I 119
Db |||
71 Q H Y K I N I C S E R S Y D V A K F R G R V A V Y P F D D H N P P T I L I Q R F C S D V D M W L K E D S S N V A V 130

QY 120 H C K A G K G R T G M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S Q R R Y V Y V Y L L 179
Db |||
131 H C K A G K G R T G M I C A Y L V F S G I K K S A D E A L A W Y D E K R T K D R K G V T I P S Q R R Y V Y V F S K L V 190

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QY 180 KNLHLYRPVALLFHKKMFETIPMFSGGTC--NPQFVVCOLKVKIYSS--NSGPTRE--- 232
D 191 CSSVPYKSVLNCVEI-----RFSSESCVQLGNVVECSISVLHDSATENAKPDLRLKTL 244
QY 233 ---DKFNFEFPQPLPVCGD 249
D 245 IDFKSVLTIKPSIPVSGD 264

RESULT 9
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AC Q9U470;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 23, Last annotation update)
DE Phosphatase and tensin homolog.
GN PTEN OR CG5671.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Perriera S., Fleischmann W.,
RA Poser C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20011294; PubMed=10542333;
RA Smith A., Smith A., Alrubale S., Coehlo C., Leever S.J., Ashworth A.;
RT "Alternative splicing of the Drosophila PTEN gene.";
RL Biochim. Biophys. Acta 1447:313-317(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R;
RX MEDLINE=20085000; PubMed=10617573;
RA Goeberdhan D.C.I., Paricio N., Goodman E.C., Mlodzik M., Wilson C.;
RT "Drosophila tumor suppressor PTEN controls cell size and number by
antagonising the Chico/Pi3-kinase signaling pathway.";
RL Genes Dev. 13:3244-3258(1999).
DR EMBL; AF003628; AAF52887.2; -
DR EMBL; AF161259; AAD45364.1; -
DR EMBL; AF201904; AAF23235.1; -
DR EMBL; AF201907; AAF23238.1; -
DR FlyBase; FBgn0026379; Pten.
DR InterPro; IPR000215; Serpin.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR000387; Tyr_phosphatase.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00506; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 506 AA; 58128 MW; 0F64D550FF35C36 CRC64;
Query Match 47.1%; Score 641.5; DB 5; Length 506;
Best Local Similarity 50.0%; Pred. No. 9.3e-55;
Matches 130; Conservative 41; Mismatches 72; Indels 17; Gaps 5;
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D 11 VIRNVSKKRIYKKGVDLTYINDNIANGYPAPDKLEGLFRNLEDVFKLEENHA 70
QY 60 NHYKYNLCARHYDTAKENCVAQPPEDHNPQLELIKPCEDLDOWLSDDNHVAI 119
D 71 QHYKYNLCSESYDVAKFRGVAVYPPDDHNPPTIELIQRCSDVDMWLKEDSNVAV 130
QY 120 HCKAGKGRGVMICAYLLHGRFLKAQEAALDFYGVETRDKGVITPISORRYVYVYL 179
D 131 HCKAGKGRGVMICAYLVFSGIKGSADEALAWYDKRTKDRGVITPISORRYVQVFSKLV 190
QY 180 KNLHLYRPVALLFHKKMFETIPMFSGGTC--NPQFVVCOLKVKIYSS--NSGPTRE--- 232
D 191 CSSVPYKSVLNCVEI-----RFSSESCVQLGNVVECSISVLHDSATENAKPDLRLKTL 244
QY 233 ---DKFNFEFPQPLPVCGD 249
D 245 IDFKSVLTIKPSIPVSGD 264

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AC Q9V3L4; Q9U468;
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Db 184 ESIKVPNRVTLKIVLRPLKPEINLSEVQFNISVGKNCVFNSEKHNMMNVWISKKKTWV 243
QY 223 SSN-SGPTREDKFN 236
Db 244 DKNKDPKPKLTKEN 258

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AC Q9LT75;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tyrosine phosphatase-like protein (Putative tyrosine
DE phosphatase).
GN AT3G19420.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Columbia;
RC Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu S., Yu S., Jones L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene At3g19420 (GI:15230379).";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025624; BAB02466.1; -
DR EMBL; AY070042; AAL49799.1; -
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00393; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 611 AA; 66430 MW; CB4FB3CFE0C6C577 CRC64;

Query Match 38.0%; Score 517; DB 10; Length 611;
Best Local Similarity 51.4%; Pred. No. 2.3e-42;
Matches 95; Conservative 31; Mismatches 51; Indels 8; Gaps 1;

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QY 55 DSKHKNHKIYNLCARHYDTAKFNCRVAQYPFEDHNPQLLELIKPFCEDLQWLSEDDN 114
Db 197 ETQHGKGYKYNLCSERLYDVSIFEGKVASFPFDDHNCPPHIVTSFCQASVSLKEDIE 256
QY 115 HVAAIHCKAGKRTGMICAYLLHKGKFLKAGALDFYGEVTRDKKGVITFSQRYVY 174
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QY 175 VSYLL 179
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Db 317 PERIL 321

Search completed: December 10, 2003, 20:34:11
Job time : 16.1874 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:28:11 ; Search time 61.1676 Seconds
(without alignments)
2496.336 Million cell updates/sec

Title: US-09-205-658A-310

Perfect score: 5168

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
- score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	507.5	9.8	565	18	AAW34402
5	507	9.8	559	20	AA107456
6	507	9.8	597	20	AA107450
7	490.5	9.5	394	20	AA107457
8	490.5	9.5	403	19	AAW64784
9	490.5	9.5	403	20	AA107462

10	490.5	9.5	403	20	AA107467	Dog MMAC1 protein.
11	490.5	9.5	403	20	AA107468	Mouse MMAC1 protei
12	490.5	9.5	403	20	AA107451	Mouse tumour suppr
13	490.5	9.5	403	20	AA107444	Human tumour suppr
14	490.5	9.5	403	20	AAW97802	Dual specificity p
15	490.5	9.5	403	21	AA180119	Human PTEN protein
16	490.5	9.5	403	22	AAU08939	Human protein phos
17	490.5	9.5	403	22	AA107452	Amino acid sequenc
18	490.5	9.5	403	22	AA107452	Amino acid sequenc
19	490.5	9.5	403	23	AA107452	Hypoxia-induced pr
20	490.5	9.5	403	23	AA107452	Human phosphoinosi
21	490.5	9.5	403	23	AA107452	Human PTEN protein
22	490.5	9.5	403	23	AA107452	Human tumour suppr
23	490.5	9.5	403	23	AA107452	Homo sapiens P-TEN
24	490.5	9.5	403	23	AA107452	Human PTEN protein
25	490.5	9.5	403	23	AA107452	Human tumour suppr
26	490.5	9.5	403	23	AA107452	Human PTEN protein
27	490.5	9.5	403	23	AA107452	Human PTEN protein
28	490.5	9.5	403	23	AA107452	Human PTEN protein
29	490.5	9.5	403	23	AA107452	Caenorhabditis ele
30	490.5	9.5	403	23	AA107452	Caenorhabditis ele
31	490.5	9.5	403	23	AA107452	Drosophila melanog
32	490.5	9.5	403	23	AA107452	Drosophila melanog
33	490.5	9.5	403	23	AA107452	Human kinase and p
34	490.5	9.5	403	23	AA107452	Amino acid sequenc
35	490.5	9.5	403	23	AA107452	Amino acid sequenc
36	490.5	9.5	403	23	AA107452	Human protein NOV1
37	490.5	9.5	403	23	AA107452	Human Tumour Endot
38	490.5	9.5	403	23	AA107452	Human tumour endot
39	490.5	9.5	403	23	AA107452	Novel human diagno
40	490.5	9.5	403	23	AA107452	Human ORFX ORF2065
41	490.5	9.5	403	23	AA107452	Human protein phos
42	490.5	9.5	403	23	AA107452	Human cytoskeleton
43	490.5	9.5	403	23	AA107452	Human cytoskeleton
44	490.5	9.5	403	23	AA107452	Human liver peptid
45	490.5	9.5	403	23	AA107452	Peptide #4513 enco

ALIGNMENTS

RESULT 1

AA13326
ID AA13326 standard; Protein; 962 AA.

AC AA13326;

XX 12-JAN-2001 (first entry)

DT Caenorhabditis elegans DAF-18.

DE Caenorhabditis elegans; daf-18; insulin signalling pathway;

DE daf-2; age-1; insulin receptor; PI 3-kinase; PKB kinase;

DE PTEN lipid phosphatase; antidiabetic; anorectic; obesity; diabetes.

XX Caenorhabditis elegans.

OS WO200033068-A1.

FN 08-JUN-2000.

PD 02-DEC-1999; 99WO-US28529.

PF 03-DEC-1998; 98US-0205658.

PR (GEHO) GEN HOSPITAL CORP.

XX Ruvkun G, Ogg S;

XX WPI; 2000-423022/36.

DR N-PSDB; AAA91623.

XX Diagnosing and treating obesity and impaired glucose tolerance using

Query Match 25.7%; Score 1330; DB 21; Length 248;
 Best Local Similarity 99.2%; Pred. No. 7.6e-105;
 Matches 246; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 48 IPTAVSSNRCTEYQNIIDLCAYITDRIIAGYPATGTEANFRNSKVQTOQFLTRRHGK 107
 1 IPTAVSSNRCTEYQNIIDLCAYITDRIIAGYPATGTEANFRNSKVQTOQFLTRRHGK 60
 108 GNVKFNLRGGYYDADNFDGNNVICFDMTDHHPSPSLELMAPFCREAKEWLEADDDKHVIAV 167
 61 GNVKFNLRGGYYDADNFDGNNVICFDMTDHHPSPSLELMAPFCREAKEWLEADDDKHVIAV 120
 168 HCKAGKGRGTGVMICALLIYINYPSPRQILDYYSIIRTKNNKGVTPSORRYIYYHKL 227
 121 HCKAGKGRGTGVMICALLIYINYPSPRQILDYYSIIRTKNNKGVTPSORRYIYYHKL 180
 228 ERELNYLPLRMOLIGVYVERPPTWGGGSKIVEVNGSTILFKPDPLIISKSNHQRERA 287
 181 ERELNYLPLRMOLIGVYVERPPTWGGGSKIVEVNGSTILFKPDPLIISKSNHQRERA 240
 288 TWLNCDT 295
 241 TWLNCDT 248

RESULT 3
 ID AAY07458
 AC AAY07458 standard; Protein; 430 AA.
 XX AAY07458;
 DT 16-JUL-1999 (first entry)
 DE Dog TS10q23.3 gene bases 1-1290 translation product.
 KW Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
 KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
 KW enzyme linked immunosorbant assay; gene expression; dog.
 XX Canis familiaris.
 OS WO9910537-A1.
 FN 04-MAR-1999.
 PD 26-AUG-1998; 98WO-US17636.
 PF 30-APR-1998; 98US-0083563.
 PR 26-AUG-1997; 97US-0057750.
 XX (MYRI-) MYRIAD GENETICS INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
 PI Yung WKA;
 DR WPI; 1999-190638/16.
 XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
 PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
 PT Syndrome and susceptibility to breast cancer
 XX Disclosure; Fig 9; 244pp; English.

CC The invention relates to mutant genes encoding the tumour suppressor
 CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
 CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
 CC gland and endometrium (claimed). The mutant gene is also useful for
 CC diagnosing a subject who has a predisposition to breast cancer. Both
 CC methods involve antibodies, which specifically bind to a TS10q23.3,
 CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.

XX

SQ Sequence 430 AA;
 Query Match 9.8%; Score 508.5; DB 20; Length 430;
 Best Local Similarity 30.3%; Pred. No. 2.3e-34;
 Matches 128; Conservative 66; Mismatches 163; Indels 65; Gaps 10;
 QY 9 PSTSTRWARDLQENPQCEPRVSEPYHNSIVVERIRHIFRTAVSSNRCTEYQNIIDLD 68
 DB 1 PPAARPGACSLRRRPRRPPLLPSLSFLSHRLPDMTAAIKKEIVSRNKRKYQEDGFOLD 60
 QY 69 CAYITDRIIAGYPATGTEANFRNSKVQTOQFLTRRHGKNNVFNLRGGYYDADNFDG 128
 DB 61 LTYIYPNLIANGFAERLEGVYRNNDVDFLSKHL-KNHYKIYNLCAERHYDTAKFNC 119
 QY 129 NVICFDMTDHHPSPSLELMAPFCREAKEWLEADDDKHVIAHCKAGKGRGTGVMICALLIYIN 188
 DB 120 RVAQYPPEDHNPQLELIKPFCELDQWLSDDNHVAIHCKAGKGRGTGVMICAYLLHRG 179
 QY 189 FYPSPRQILDYYSIIRTKNNKGVTPSORRYIYYHKLREELNYLPLRMOLIGVYVERP 248
 DB 180 KFLKAQAEALDFYGEVTRDKKGVTPSORRYIYYHKLREELNYLPLRMOLIGVYVERP 239
 QY 249 PKTWGGGSKIVEVNGSTILFKPDPLIISKSNHQRERATWLNCDTNEFDTGOKYHG 308
 DB 240 PMFSGG-----TCNPOFVVCQKVKIYNSNSGPTTR-----EDKF-- 274
 QY 309 FVSKRAYCFMVPEDAPVVEGDVIRIDI--REIGFLKFFSDGKIGHVWFNTMF----- 358
 DB 275 -----MYFEFPQPLPVC--GDIKVERPHKQNKMLKK--DKMFHFVWNTFFIPGPEETS 323
 QY 359 -----ACDGLNG-GHFEYVDKTPYIGDDTSIGRKNGRNRNETPMRKIDPETGNEFE 410
 DB 324 EKVENGSLCDOEIDISICIERADNDKEYL-----VLTLTKNDLKANKKANKRYF 373
 QY 411 SP 412
 DB 374 SP 375
 RESULT 4
 ID AAW34402 standard; Protein; 565 AA.
 XX AAW34402;
 AC AAW34402;
 DT 06-MAR-1998 (first entry)
 DE Protein encoded by gene of IMAGE clone 264611.
 XX IMAGE clone 264611; gene fragment; human; chromosome 10; D10S541 marker;
 KW D10S215 marker; tumour suppressor gene; prostatic cancer; cancer therapy;
 KW melanoma; glioma; non-Hodgkin's lymphoma; cancer susceptibility;
 KW diagnosis; prognosis; mutation detection; suppressor gene; neoplasia;
 KW hyperplasia; 10q loss tumour.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 484
 FT /label= unknown
 FT /note= "encoded by RAA"
 XX
 PN WO9715686-A1.
 XX
 PD 01-MAY-1997.
 XX
 PF 22-OCT-1996; 96WO-GB02588.
 XX
 PR 23-OCT-1995; 95US-0005840.
 XX
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 XX
 PI Gray IC, Spurr NK;

XX WPI: 1997-259037/23.
 DR N-PSDB; AAT93354.
 XX
 PT Nucleic acid hybridizing to chromosome 10 tumour suppressor gene -
 PT useful for diagnosis, prognosis and treatment of prostatic cancer
 PT and for assessing susceptibility to cancer
 XX
 PS Claim 20; Fig 7; 127pp; English.
 XX
 CC This sequence represents the protein encoded by the cDNA of the gene
 CC from the IMAGE clone 264611. The cDNA sequence, and the sequences of its
 CC exons (see AAT93326-793333) are all nucleic acid sequences of the
 CC invention. The nucleic acid of the invention (I) is able to hybridise
 CC selectively to the region of human chromosome 10 bounded by the markers
 CC D10S541 and D10S215. (I) is a tumour suppressor gene, particularly
 CC involved in prostatic cancer but also in melanoma, glioma and
 CC non-Hodgkin's lymphoma. Any nucleic acid that hybridises selectively to
 CC the specified chromosomal region can be used to determine susceptibility
 CC of a patient to cancer and for diagnosis/prognosis, especially of
 CC prostatic cancer, i.e. by detecting mutations. The wild-type suppressor
 CC gene can also be used to treat cancer, especially when included in a
 CC viral vector. Similar detection methods can be based on the amount of
 CC protein encoded by (I), or its truncation or loss, in a sample,
 CC particularly using labelled molecules capable of hybridising to the
 CC protein, particularly antibodies. The labelled molecules when coupled to
 CC a cytotoxin can be used for cancer treatment. The encoded protein can be
 CC used to raise antibodies and these used to screen DNA expression
 CC libraries or for polypeptide isolation. (I) allows differential diagnosis
 CC between neoplasia and hyperplasia of the prostate (all tumours with a 10q
 CC loss have lost this region) and determination of micro-metastases in the
 CC blood.
 XX
 SQ Sequence 565 AA;
 Query Match 9.8%; Score 507.5; DB 18; Length 565;
 Best Local Similarity 31.2%; Pred. No. 4.4e-34;
 Matches 130; Conservative 66; Mismatches 159; Indels 61; Gaps 11;
 QY 10 STSTRMARD-LOENPNRQGPVSEPYHNSIVERIRHIFRTAVSSNRCRTEYQNDID 68
 DB 127 SATAKSRAISILQKKPRHQQLPSLSFFSHRLPDMTAKIKEIVSNRKRYYQEDGFDLD 186
 QY 69 CAYITDRIIAGYPATGIEANFRNSKVQTOQLTRRHGKGNVFNLRGGYYVDADNPDG 128
 DB 187 LTYIYPNIIANGFPAERLEGVYRNNDVVRFLDSKH-KNHYKIYNLCARHYDTAKENC 245
 QY 129 NVICFDMTDHPPSLEMAPPCREAKEWLEADKHVIAVHCAGKGRGTGMICALLIYN 188
 DB 246 RVAQYPPFDHNPQLEIKPFCELDQWLSDDNHVAIHCAGKGRGTGMICALLHRG 305
 QY 189 FVPSRQILDYYSIIRTKNKGVTIPSORRYIYYHYKLRERELNVLPLRMQLIGVYVERP 248
 DB 306 KFLKAQEAIDFYGEVTRDKKGVTPSORRYIYYHYKLRERELNVLPLRMQLIGVYVERP 365
 QY 249 PKTWGGGSKIKVEVNGSTILFKPDPPLIISKNHQERATWLNCDTPNEFTGQKYHG 308
 DB 366 PMFSGG-----TCNPQFVVCQKLVKIISSNSGPTTR-----EDKF-- 400
 QY 309 FVSKRAYCFMVPEDAPVFEVGDVRIDI--REIGFLKKFSDGKIGHVWNTMF----- 358
 DB 401 -----MYFEFPQLPVC--GDIKVEFFHKQNKMLK---DKMFHFWNTTFFPGPEETS 449
 QY 359 -----ACDGLNG-GHFEYVDKTPYI-----GDDTSIGRKNGRNRNETPMRKI 401
 DB 450 EKVENGLCQDIBDSICSIERADNDKEYLVLTXTNDLDKANKDKANRYFSPNFV 505
 RESULT 5
 AAY07456
 ID AAY07456 standard; peptide; 559 AA.
 XX
 AC AAY07456;

XX 16-JUL-1999 (first entry)
 DT Mouse TS10q23.3 gene bases 283-1959 translation product.
 XX
 DE Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
 KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
 KW enzyme linked immunosorbant assay; gene expression; mouse.
 XX
 OS Mus musculus.
 XX
 XX WO9910537-A1.
 XX
 PD 04-MAR-1999.
 XX
 PF 26-AUG-1998; 98WO-US17636.
 XX
 PR 30-APR-1998; 98US-0083563.
 PR 26-AUG-1997; 97US-0057750.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
 PI Yung WKA;
 XX
 DR WPI; 1999-190638/16.
 XX
 XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
 PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
 PT Syndrome and susceptibility to breast cancer
 PT
 XX Disclosure; Fig 9; 244pp; English.
 XX
 CC The invention relates to mutant genes encoding the tumour suppressor
 CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
 CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
 CC gland and endometrium (claimed). The mutant gene is also useful for
 CC diagnosing a subject who has a predisposition to breast cancer. Both
 CC methods involve antibodies, which specifically bind to a TS10q23.3,
 CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
 XX
 SQ Sequence 559 AA;
 Query Match 9.8%; Score 507; DB 20; Length 559;
 Best Local Similarity 30.6%; Pred. No. 4.7e-34;
 Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;
 QY 10 STSTRMARD-LOENPNRQGPVSEPYHNSIVERIRHIFRTAVSSNRCRTEYQNDID 68
 DB 121 SATAKSRAISILQKKPRHQQLPSLSFFSHRLPDMTAKIKEIVSNRKRYYQEDGFDLD 180
 QY 69 CAYITDRIIAGYPATGIEANFRNSKVQTOQLTRRHGKGNVFNLRGGYYVDADNPDG 128
 DB 181 LTYIYPNIIANGFPAERLEGVYRNNDVVRFLDSKH-KNHYKIYNLCARHYDTAKENC 239
 QY 129 NVICFDMTDHPPSLEMAPPCREAKEWLEADKHVIAVHCAGKGRGTGMICALLIYN 188
 DB 240 RVAQYPPFDHNPQLEIKPFCELDQWLSDDNHVAIHCAGKGRGTGMICALLHRG 299
 QY 189 FVPSRQILDYYSIIRTKNKGVTIPSORRYIYYHYKLRERELNVLPLRMQLIGVYVERP 248
 DB 300 KFLKAQEAIDFYGEVTRDKKGVTPSORRYIYYHYKLRERELNVLPLRMQLIGVYVERP 359
 QY 249 PKTWGGGSKIKVEVNGSTILFKPDPPLIISKNHQERATWLNCDTPNEFTGQKYHG 308
 DB 360 PMFSGG-----TCNPQFVVCQKLVKIISSNSGPTTR-----EDKF-- 394
 QY 309 FVSKRAYCFMVPEDAPVFEVGDVRIDI--REIGFLKKFSDGKIGHVWNTMF----- 358
 DB 395 -----MYFEFPQLPVC--GDIKVEFFHKQNKMLK---DKMFHFWNTTFFPGPEETS 443
 QY 359 -----ACDGLNG-GHFEYVDKTPYI-----GDDTSIGRKNGRNRNETPMRKIDRETGNEFE 410

```
Db 444 EKVENGLCDQDEIDSICSIERADNDKEYL-----VLTLTKNLDKANKOKANRYF 493
Qy 411 SP 412
Db 494 SP 495

RESULT 6
AA07450
ID AA07450 standard; peptide; 597 AA.
AC AA07450;
XX
XX
XX 16-JUL-1999 (first entry)
DT
DE Human TS10q23.3 gene bases 453-2243 translation product.
KW Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
KW enzyme linked immunosorbant assay; gene expression; human.
XX
XX Homo sapiens.
XX
XX WO9910537-A1.
XX
XX 04-MAR-1999.
XX
XX 26-AUG-1998; 98WO-US17636.
XX
XX 30-APR-1998; 98US-0083563.
XX 26-AUG-1997; 97US-0057750.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
XX Yung WKA;
XX
XX WPI; 1999-190638/16.
XX
XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
XX suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
XX Syndrome and susceptibility to breast cancer
XX
XX Disclosure; Fig 9; 244pp; English.
XX
XX The invention relates to mutant genes encoding the tumour suppressor
XX TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
XX Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
XX gland and endometrium (claimed). The mutant gene is also useful for
XX diagnosing a subject who has a predisposition to breast cancer. Both
XX methods involve antibodies, which specifically bind to a TS10q23.3,
XX used in an ELISA assay to evaluate the level of TS10q23.3 expression.
XX
XX Sequence 597 AA;
XX
XX Query Match 9.8%; Score 507; DB 20; Length 597;
XX Best Local Similarity 30.6%; Pred. No. 5.2e-34;
XX Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;

Qy 10 STSTRSMARD-LQENFNQGEPRVSEPYHNSIVERIRHIFRTAVSSNRCRTEYQNIIDL 68
Db 159 SATAKSRAISILQKPRHQQLPSLSPPFFSHRLPDMTALIKEIVSNKRRYQEDGFDLD 218
Qy 69 CAYITDRIIAGYPATGIEANFRNSKVQOQLTRRHGKGNVFNRLGGYVYDADNPDG 128
Db 219 LTYIYFNIIAMGPAERLEGVYRNNDIDVVRFLDSKH-KNHYKIYNLCAERHYDTAKFNC 277
Qy 129 NVICDMTDHHPHLEMAFFCREAKWLEADKKVIAVHCAGKAGRTGVMICALLIYN 188
Db 278 RVAQYPFEDHNPQELIKPFCELDLQWLSUEDDNHVAIHCAGKAGRTGVMICALLHRG 337

Qy 189 FYPSPROILDYYSIIRTKNNKGVTPISORRYVYYHKLREELNYLPLRMOLIGVYVERP 248
Db 338 KFLQAQEAALDFYGEVTRDKKGVTPISORRYVYYHKLREELNYLPLRMOLIGVYVERP 397
Qy 249 PKTWGGGSKIKEVEGVNGSTILFKPDPLIISKSNHQRERATWLNNCDDTNEFDTGQKYHG 308
Db 398 PMFSGG-----TCNQFVVVQOLVKVIYSSNSGPTTR-----EDKF-- 432
Qy 309 FVSKRAYCFMVPEDAPVVEGDVRIDI--REIGFLKKFSDGKI GHVWNTWTF----- 358
Db 433 -----MYFEPFQPLPVC--GDIKVEPFHKQKMLKK--DKMFHFVWNTFFIPGPEETS 481
Qy 359 -----ACDGLNG-GHFEYVDTQPYIGDDTSIGRKNGRNETPMRKIDPETGNEFE 410
Db 482 EKVENGLCDQDEIDSICSIERADNDKEYL-----VLTLTKNLDKANKOKANRYF 531
Qy 411 SP 412
Db 532 SP 533

RESULT 7
AA07457
ID AA07457 standard; Protein; 394 AA.
XX
XX AC AA07457;
XX
XX 16-JUL-1999 (first entry)
DT
DE Dog tumour suppressor protein TS10q23.3.
XX
XX Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
XX Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
XX enzyme linked immunosorbant assay; gene expression; dog.
XX
XX Canis familiaris.
XX
XX WO9910537-A1.
XX
XX 04-MAR-1999.
XX
XX 26-AUG-1998; 98WO-US17636.
XX
XX 30-APR-1998; 98US-0083563.
XX 26-AUG-1997; 97US-0057750.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
XX Yung WKA;
XX
XX WPI; 1999-190638/16.
XX N-PSDB; AAX57673.
XX
XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
XX suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
XX Syndrome and susceptibility to breast cancer
XX
XX Disclosure; Fig 9; 244pp; English.
XX
XX The invention relates to mutant genes encoding the tumour suppressor
XX TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
XX Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
XX gland and endometrium (claimed). The mutant gene is also useful for
XX diagnosing a subject who has a predisposition to breast cancer. Both
XX methods involve antibodies, which specifically bind to a TS10q23.3,
XX used in an ELISA assay to evaluate the level of TS10q23.3 expression.
XX
XX Sequence 394 AA;
XX
XX Query Match 9.5%; Score 490.5; DB 20; Length 394;
XX Best Local Similarity 31.3%; Pred. No. 7e-33;
```

Matches	120; Conservative	60; Mismatches	138; Indels	65; Gaps	10;
Qy	48	IFTAVSSNCRTEYQNIIDLCAVITDRIITAIGYPATGIEANPRNSKVQCOQLTRRHGK	107		
Db	4	I I K E I V S R N K R R Y Q E D G F D J D L T V I Y N I I A M G P P A E R L E G V G Y R N N I D D V V R F D L S K H - K	62		
Qy	108	GNVKVFNLRGGYVVDADNFDGNCVFCFOWTDHHPSSLMAFPFCEAKEWLEADDKHVIIV	167		
Db	63	NHYKIYNLCABRHYDIAKFCNRAVQYFEDHNPQLELIKPFCEDLQWLSEDDNHVAAI	122		
Qy	168	HKAGKGRGTGMICALLIYINFPSRQIIDLYSIIIRTKNKGVTIIPSQRRYIYYHKLK	227		
Db	123	HKAGKGRGTGMICAYLLHKGKFLKAGEALDFYGEVETRDKGVTIIPSQRYIYYSYLL	182		
Qy	228	ERELNYLPLRMQLIGVYVERPPKTGWGGSKIKVEGVNGSTILFKPDPILIISKSHQERA	287		
Db	183	KNHLDYRVPVALLFHKMMFETIPMSGG-----TCNPQFVVCOLKVKIYSSNSGPTFR-	234		
Qy	288	TWLNCCDTPNEFDTGEQYHGFVSKRAYCFMVPEDAPVFVEGDVRIDI--REIGFLKKFS	345		
Db	235	-----EDKF-----MYTEFPQPLPVC--GDIKVEFFHKQNKWLK--	267		
Qy	346	DGKIGHVWFNTMF-----ACDGLNG-GHFEYVDKTPQYIGDDTSIGRKN	389		
Db	268	-DKMFHFVWNTFFIPGPPEETSEKVENGLCDQEDISCSIERADNDKEYL-----	316		
Qy	390	GMRNETPMRKIDPDTGNFESP	412		
Db	317	VLTLTKNDLKDANKDKANRYFSP	339		

RESULT 8	
AAW64784	
ID	AAW64784 standard; Protein; 403 AA.
XX	
AC	AAW64784;
XX	
DT	03-NOV-1998 (first entry)
XX	
XX	Human tumour suppressor TS10q23.3 protein.
DE	
XX	
XX	Tumour suppressor; TS10q23.3; human; diagnosis; tumour; prostate; breast;
KW	brain; glioma; metastasis; gene therapy; anti-cancer; transgenic animal;
KW	drug screening.

Tumour suppressor TS10q23.3 and related antibodies - useful for
 diagnosis, staging and treatment of cancer, especially of breast,
 prostate and brain
 Claim 1; Fig 7; 161pp; English.
 This sequence represents the human tumour suppressor protein TS10q23.3.
 This protein can be used to diagnose a wide range of tumours,
 particularly of prostate, breast and brain (glioma), to stage cancers

CC (particularly differentiation between low grade brain cancer and glioma) and for prediction of metastasis. This suppressor and its nucleic acid CC are also used to alter the phenotype to specifically treat cancer cells, CC are also used to alter the phenotype to specifically treat cancer cells, CC e.g. by in vivo or ex vivo gene therapy, optionally together with other CC anti-cancer agents. Fragments of the suppressor can be coupled to an CC immunogenic carrier and are used to raise antibodies, to isolate CC antigens, as immunoassay reagents, to clone related DNA or for CC immunotherapy. Antisense nucleic acid can be used to produce transgenic CC animals (useful for drug screening) or to eliminate dominant negative CC mutants.

Ax	SQ	Sequence	403 Aa;
		Query Match	9.5%; Score 490.5; DB 19; Length 403;
		Best Local Similarity	31.3%; Pred. No. 7.2e-33;
		Matches 120; Conservative	60; Mismatches 138; Indels 65; Gaps 10
Qy	Db	48 IFTAVSNRCRTEYQNIDLCAYITDRIITAIGYPATGTEANFRNSKVOTQQFLTRHGK	107
		: : : : : : : : : : : : : : : : : :	:
Db		4 IIKEIVSRNKRYQEODGLDLTLTYINIIAMGFPAERLEGVVRNNDIDDVFLOSKH-K	62
		: : : : : : : : : : : : : : : : : :	:
Qy	Db	108 GNVKVNLRGGYYIDAONFCDNVICFDMTDHPFPSELMAFFCREAKEWLEADDKHVIATV	167
		: : : : : : : : : : : : : : : : ~:	:
Db		63 NHYKIYNLCASRHVDYTAKENCRVAQYPFEDHNPPQLLEIKPFCEDLDQMLEDNNHAAI	122
		: : : : : : : : : : : : : : : : : :	:
Qy	Db	168 HCKAGKGRTGYMICALLIYNFYPSPRQILDYSIIRTKNNGVTIPTSORRYIYYHKLR	227
		: : : : : : : : : : : : : : : : : :	:
Db		123 HCKAGKGRTGYMICYLLHRGKFLEAALDFGEVRTDKKGVTIPTSORRYIYYLYL	182
		: : : : : : : : : : : : : : : : : :	:
Qy	Db	228 ERELNYELRLMQLGTVVERPPKTGWGGSKIKEVGNGSTILFKPDPLIISKSNHQRERA	287
		: : : : : : : : : : : : : : : : : :	:
Db		183 KNHLDYRPVALLFPHKMFEIIPMFESG-----TCNPQVVQLAKVIYSSNSGPTR-	234
		: : : : : : : : : : : : : : : : : :	:
Qy	Db	288 TWLNCDTPNEFDTGEOKYGHGVFSKRAYCFMWPEADAPVEGDVIRDI--REIGFLKKFS	345
		: : : : : : : : : : : : : : : : : :	:
Db		235 -----EDKF-----MYEFPQLPVC--GDIKVEFHQKNMLKK--	267
		: : : : : : : : : : : : : : : : : :	:
Qy	Db	346 DGKIGHVWFNTMF-----ACDGGING-GHFVEYDKTQPYGDDTSIGRN	389
		: : : : : : : : : : : : : : : : : :	:
Db		268 -DKMHFWNTFFFPGPEETSEKVENGSLCDQSIDSCSIERADNDKEYL-----	316
		: : : : : : : : : : : : : : : : : :	:
Qy	Db	390 GMRNETPMRKIDPETGNFESP	412
		: : : : : : : : : : : : : : : : : :	:
Db		317 VLTLTKNDLDRKANRKYFSP	339

RESULT 9	
AAAY07462	
ID	AAAY07462 standard; peptide; 403 AA.
XX	
AC	AAAY07462;
XX	
DT	16-JUL-1999 (first entry)
XX	
DE	Mouse MMAC1 protein sequence.
XX	
KW	Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
KW	Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
KW	enzyme linked immunosorbant assay; gene expression; mouse.
XX	
OS	Mus musculus.
XX	
PN	WO9910537-Al.
XX	
PD	04-MAR-1999.
XX	
PF	26-AUG-1998; 98WO-US17636.
XX	
PR	30-APR-1998; 98US-0083563.
XX	
PR	26-AUG-1997; 97US-0057750.
XX	
PA	(MYRI-) MYRIAD GENETICS INC.
PA	(TEXA) UNIV TEXAS SYSTEM.


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04-MAR-1999.
XX XX
XX XX      98WO-US17636.
XX XX
XX XX
XX XX
XX XX      98US-0083563.
XX XX
XX XX      97US-0057750.
XX XX
XX XX      (MYRI-) MYRIAD GENETICS INC.
XX XX      (TEXA ) UNIV TEXAS SYSTEM.
XX XX
XX XX
XX XX      Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
XX XX      Yung WKA;
XX XX
XX XX      WPI; 1999-190638/16.
XX XX
XX XX      N-PSDB; AAX57699.
XX XX
XX XX      Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
XX XX      suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
XX XX      Syndrome and susceptibility to breast cancer
XX XX
XX XX      Claim 3; Page 232-233; 244pp; English.
XX XX
XX XX      The invention relates to mutant genes encoding the tumour suppressor
XX XX      TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
XX XX      Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
XX XX      gland and endometrium (claimed). The mutant gene is also useful for
XX XX      diagnosing a subject who has a predisposition to breast cancer. Both
XX XX      methods involve antibodies, which specifically bind to a TS10q23.3,
XX XX      used in an ELISA assay to evaluate the level of TS10q23.3 expression.
XX XX
XX XX      Sequence      403 AA;
XX XX
XX XX      Query Match      9.5%; Score 490.5; DB 20; Length 403;
XX XX      Best Local Similarity 31.3%; Pred. No. 7.2e-33;
XX XX      Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
XX XX
XX XX      Qy      48 IFTAVSSNRCRTYEQNIIDLCAYITDRIIAIGYPATGIEANFRNSKVQTFQFLTRHGK 107
XX XX      Db      4 I I K E I V S R N K R R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H - K 62
XX XX
XX XX      Qy      108 G N V K V N L R G G Y Y D A D N P D G N V I C F D M T D H P P S L E M A P F C R A K E W L E A D D K H V I A V 167
XX XX      Db      63 N H Y K I Y N L C A E R H Y D A K F N C R V A Q P F F D H N P P Q L E I K P F C E D L D Q W L S E D D N H V A A I 122
XX XX
XX XX      Qy      168 H C K A G R G T G V M I C A L L I Y I N F P S P R Q I L D Y V S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 227
XX XX      Db      123 H C K A G R G T G V M I C A L L H R G E L K Q A E L D F V G E V R T D K G V T I P S O R Y V Y Y S Y L L 182
XX XX
XX XX      Qy      228 E R E I N L P L R M L I G V V Y E R P P T T W G G S K I K V E G N G S T I L F K P D L I I S K N H O R E R A 287
XX XX      Db      183 K N H L D Y R P V A L L F H K M W F E T I P M F S G G - - - - - T C N P Q V V C Q L K V I Y S S N S G P T R R - 234
XX XX
XX XX      Qy      288 T W L N C D T P N E F D T G Q K Y H G F V S K R A Y C P M V P E D A P V F V E G D V R I D I - - R E I G F L K K F S 345
XX XX      Db      235 - - - - - E D K F - - - - - M Y E F F Q P L P V C - - G D I K V E F F H Q K M L K K - - 267
XX XX
XX XX      Qy      346 D G K I G H W F N T M P - - - - - A C D G L G I N G - G H F E Y D K T Q P Y I G D D T S I G R K N 389
XX XX      Db      268 - D K W F H F W N T F I P G P E E T S E K V E N G S L C D Q E I D S I C S I E R A D N D K E Y L - - - - - 316
XX XX
XX XX      Qy      390 G M R N E T P M R K I D P E T G N E F S P 412
XX XX      Db      317 V L I L T K N D L D K A N K D K A N R Y F S P 339
XX XX
XX XX      RESULT 11
XX XX      AAY07468
XX XX      ID      AAY07468 standard; Protein; 403 AA.
XX XX
XX XX      AAY07468;
XX XX
XX XX      16-JUL-1999 (first entry)
XX XX

```

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DE Mouse MMAC1 protein.
XX Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
XX enzyme linked immunosorbant assay; gene expression; mouse.
OS Mus musculus.
XX WO9910537-A1.
XX 04-MAR-1999.
XX *26-AUG-1998; 98WO-US17636.
XX 30-APR-1998; 98US-0083563.
PR 26-AUG-1997; 97US-0057750.
XX (MYRI-) MYRIAD GENETICS INC.
PA (TEXA) UNIV TEXAS SYSTEM.
XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
PI Yung WKA;
XX WPI; 1999-190638/16.
DR N-PSDB; AAX57700.
XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
PT Syndrome and susceptibility to breast cancer
XX Disclosure; Page 236-238; 244pp; English.
XX The invention relates to mutant genes encoding the tumour suppressor
CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
CC gland and endometrium (claimed). The mutant gene is also useful for
CC diagnosing a subject who has a predisposition to breast cancer. Both
CC methods involve antibodies, which specifically bind to a TS10q23.3,
CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
XX Sequence 403 AA;
SQ
Query Match 9.5%; Score 490.5; DB 20; Length 403;
Best Local Similarity 31.3%; Pred. No. 7.2e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
QY 48 IFRVAVSSNRCTEYQNIIDLCAYITDRIIAIGYPATGCIANFRNSKVQTOQFLTRRHGK 107
DB 4 IIKEIVSRNKRKYQEDGFDLDLTYYIPNIIAMGPPAERLEGVYRNNDVVRFDSKH-K 62
QY 108 GNVKVNLRGGYYVDADNFDGNVICFDMTDHHPSPLELMAPFCREAKEWLEADDKHVIATV 167
DB 63 NHYKIYNLCARHYDTAKFNCRAQYPPFDHNPQLELIKPFCELDQWLSDDNHVAI 122
QY 168 HCKAGKGRGVMICALLIYINFPSPRQILDVYSIIRTKNNKGVITIPSORRYIYYHKLK 227
DB 123 HCKAGKGRGVMICAYLLHRGKFLKAQEBALDFYGEVTRDKKGVITIPSORRYIYYSVLL 182
QY 228 ERELNYLPLRMQLIGVYVERPPTKGGGSKI KVEVNGNSTILFKPDDPLIISKSNHQRERA 287
DB 183 KNLHLYRPVALLFHKKMFETIPMFSGG-----TCNPQFVVCQLKVIYSSNGPTRR- 234
QY 288 TWLNCDTNEFDTEGQKHGKVFVSKRAYCFMVPEADPVFVEGDVRIDI--REIGFLKKFS 345
DB 235 -----EDKP-----MYFEFPQPLPVC--GDIKVEFPFHKKQMLKK-- 267
QY 346 DGKIGHWNTMF-----ACDGLNG-GHFEVVDKTPQVIGDTSIGRKN 389
DB 268 -DKMFHWNTFIPCPETSEKVENGLCDQEISIERADNDKEYL----- 316
QY 390 GMRNETPMRKIDPETGNFEFSP 412
DB 317 VLTLTKNLDLKANKDKANRYFSP 339

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Db 235 -----EDKF-----MYFFPQPLPVC--GDIVKVEFFHKONKMLKK-- 267
 QY 346 DGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIGDTSIGRKN 389
 Db 268 -DKMFHWNTFFIPGPEETSEKVENGLSCQDEIDSICSIERADNDKEYL----- 316
 QY 390 GMRNETPMRKIDPETGNEFESP 412
 Db 317 VLTLTKNDLKDANKDKANRYFSP 339

RESULT 13
 AAY07444
 ID AAY07444 standard; Protein; 403 AA.
 AC AAY07444;
 XX
 XX 16-JUL-1999 (first entry)
 XX Human tumour suppressor protein TS10q23.3.
 DE Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
 KW Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
 KW enzyme linked immunosorbent assay; gene expression; human.
 XX
 OS Homo sapiens.
 XX
 XX WO9910537-A1.
 XX
 XX 04-MAR-1999.
 XX
 XX 26-AUG-1998; 98WO-US17636.
 XX
 XX 30-APR-1998; 98US-0083563.
 PR 26-AUG-1997; 97US-0057750.
 XX
 XX (MYRI-) MYRIAD GENETICS INC.
 PA (TEXA-) UNIV TEXAS SYSTEM.
 XX
 XX Jasser SA, Pershouse MA, Steck P, Tavtigian SV;
 PI Yung WKA;
 XX
 XX WPI; 1999-190638/16.
 DR N-PSDB; AAX57671.
 XX
 XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
 PT suppressor (TS10q23.3); useful for the diagnosis of Cowden's
 PT Syndrome and susceptibility to breast cancer
 XX
 PS Disclosure; Fig 7; 244pp; English.
 XX
 XX The invention relates to mutant genes encoding the tumour suppressor
 CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
 CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
 CC gland and endometrium (claimed). The mutant gene is also useful for
 CC diagnosing a subject who has a predisposition to breast cancer. Both
 CC methods involve antibodies, which specifically bind to a TS10q23.3,
 CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.

Sequence 403 AA;
 Query Match 9.5%; Score 490.5; DB 20; Length 403;
 Best Local Similarity 31.3%; Pred. No. 7.2e-33;
 Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
 QY 48 IFTAVSNCRTEYQNDLDCAYITDRIIATGYPATGIEANFRNSKVQTOQFLRRHGK 107
 Db 4 IIEIVSNKRKYQEDGDLDTIYVPNIAMGFAERLEGVYRNIDVVRFLDSKH-K 62
 QY 108 GNVKVPNLRGGYYADADPDGNCVCFDTHDHPSPLELMAPPCEAKWLEADDGHVIAV 167
 Db 63 NHYKIYNLCARHRYDTAKFNCRVAQYPPFEDHNPPQLEIKPFCDLDQWLSDDDNHA 122

QY 168 HCKAGKGTGMICALLIYINFPSPRQILDYVGIIRTKNNKGVITPSQRRIYYHKLK 227
 Db 123 HCKAGKGTGMICAYLLHRGKFLKAQEALEDFGEVTRDKKGVITPSQRRIYYHKLK 182
 QY 228 ERELNYLPLRMQLIGVVVERPKTWGGGSKIKVEGNGSTILFKPDPDLIISSKNHQRERA 287
 Db 183 KNHLDYRPVALLFHMMFETIPMFSGG-----TCNPFQVVCQKVKIYSSNGPTRR- 234
 QY 288 TLLNCDTPNEFDTEQKYGHFVSKRAYCFMVPEADPVFVEGDVRI--REIGFLKKFS 345
 Db 235 -----EDKF-----MYFFPQPLPVC--GDIVKVEFFHKONKMLKK-- 267
 QY 346 DGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIGDTSIGRKN 389
 Db 268 -DKMFHWNTFFIPGPEETSEKVENGLSCQDEIDSICSIERADNDKEYL----- 316
 QY 390 GMRNETPMRKIDPETGNEFESP 412
 Db 317 VLTLTKNDLKDANKDKANRYFSP 339

RESULT 14
 AAW97802
 ID AAW97802 standard; Protein; 403 AA.
 AC AAW97802;
 XX
 XX 21-MAY-1999 (first entry)
 XX Dual specificity phosphatase PTEN.
 DE PTEN; MMAC1; protein tyrosine phosphatase; human; prostate cancer;
 KW brain cancer; prostate cancer; tumour suppressor; Cowden's disease;
 KW neurodegenerative disease; Parkinson's disease; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO9902704-A2.
 XX
 XX 21-JAN-1999.
 XX
 XX 08-JUL-1998; 98WO-US14205.
 XX
 XX 29-JUN-1998; 98US-0090984.
 PR 08-JUL-1997; 97US-0051908.
 XX
 XX (COLD-) COLD SPRING HARBOR LAB.
 PA
 XX
 PI Myers MP, Tonks NK;
 XX
 XX WPI; 1999-120905/10.
 DR N-PSDB; AAX07339.
 XX
 XX New use of PTEN phosphatase - for developing products for the
 PT diagnosis and treatment of hyperproliferative disorders, e.g.
 PT cancers or neurodegenerative disorders such as Parkinson's disease
 XX
 PS Disclosure; Fig 1A-C; 60pp; English.
 XX
 XX This is the amino acid sequence of human PTEN phosphatase,
 CC predicted from the PTEN gene (see AAX07339) located at 10q22-23.
 CC PTEN shares homology with the protein tyrosine phosphatase in
 CC family. It can function as a dual specificity phosphatase in
 CC vitro, displaying selectivity for extremely acidic substrates.
 CC PTEN dephosphorylates phosphatidylinositol in vitro, and displays
 CC selectivity for the 3 position of the inositol ring. It is also
 CC able to dephosphorylate serine, threonine and tyrosine residues
 CC when present in acidic substrates. The phosphatase activity of
 CC PTEN is required for its ability to function as a tumour suppressor
 CC or an apoptosis inducer. Point mutations, including point mutations
 CC in tumour samples and Cowden's disease kindreds, ablate PTEN
 CC activity. PTEN functions as an upstream, negative regulator of

CC PKB/Akt and has the potential to regulate signals associated with
 CC control of cell survival. PTEN polypeptides and polynucleotides
 CC can be used in the diagnosis and treatment of conditions
 CC characterised by an alteration in PTEN which causes an alteration
 CC of phosphatase activity. They can be used to treat
 CC hyperproliferative conditions such as cancers, e.g. brain, prostate
 CC or breast cancers or Cowden's disease, or other hyperproliferative
 CC diseases involving reduced phosphatase activity. They can also be
 CC used in methods of reducing PTEN phosphatase activity for treating
 CC conditions such as Parkinson's disease and other neurodegenerative
 CC disease.
 XX
 XX
 SQ *Sequence 403 AA;
 Query Match 9.5%; Score 490.5; DB 20; Length 403;
 Best Local Similarity 31.3%; Pred. No. 7.2e-33;
 Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
 QY 48 IFTAVSSNRCTEQYQNDLDCAYITDRIIAIGYPATGIEANFRNSKVQTOQLTRRHGK 107
 Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H - K 62
 QY 108 G N V K F N L R G G Y Y D A N D F G N V I C F D M T D H P P S L E M A P F C R E A K E W L E A D D K H V I A V 167
 Db 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A I 122
 QY 168 H C K A G K R T G V M I C A L L I Y I N F P S P R Q I L D Y S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 227
 Db 123 H C K A G K R T G V M I C A L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y I Y Y S Y L L 182
 QY 228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E G N G S T I L F K P D P L I I S K S N H Q R E R A 287
 Db 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G ----- T C N P Q F V V C Q L K V I Y S N S G P T R R - 234
 QY 288 T W L N N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I - - R E I G F L K K F S 345
 Db 235 ----- E D K F ----- M Y F E F P Q P L P V C - - G D I K V E F F H K Q N K M L K K - - 267
 QY 346 D G K I G H V W F N T M P ----- A C D G G L N G - G H F E Y V D K T Q P Y I G D D T S I G R K N 389
 Db 268 - D K M F H F W N T F F I P G P E E T S E K V E N G S L C D Q E I D S I C S I E R A D N D K E Y L ----- 316
 QY 390 G M R R N E T P M R K I D P E T G N E F E S P 412
 Db 317 V L T L T K N D L D K A N K A N R Y F S P 339
 RESULT 15
 ID AAY80119 standard; Protein; 403 AA.
 AC AAY80119;
 XX
 XX 22-MAY-2000 (first entry)
 XX
 XX Human PTEN protein sequence SEQ ID NO:1.
 XX
 KW Human; PTEN; MMAC1; TEPI; phosphorothioate; antisense oligonucleotide;
 KW inhibition; protein phosphatase; tumour; diagnosis; inflammation;
 KW anticancer; anti-inflammatory; anti-infective; infection.
 XX
 OS Homo sapiens.
 XX
 PN US6020199-A.
 XX
 PD 01-FEB-2000.
 XX
 PF 21-JUL-1999; 99US-0358381.
 XX
 PR 21-JUL-1999; 99US-0358381.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX

PI Monia BP, Cowser LM;
 XX
 XX WPI; 2000-181363/16.
 DR N-PSDB; AAZ91361.
 XX
 PT New antisense compounds useful for treating, preventing or diagnosing
 PT e.g. tumors or inflammation, are targeted to the human dual specificity
 PT protein phosphatase (PTEN) sequence -
 XX
 XX Claim 1; Column 43-46; 32pp; English.
 XX
 CC The present invention describes phosphorothioate antisense
 CC oligonucleotides that are targeted to the 3'-untranslated region (UTR)
 CC of the sequence encoding a human dual specificity protein phosphatase
 CC designated PTEN (also known as MMAC1 and TEPI), and hybridise
 CC specifically to the human PTEN nucleotide sequence given in AAZ91361.
 CC The antisense oligonucleotides have anticancer, anti-inflammatory and
 CC anti-infective activities. The phosphorothioate antisense
 CC oligonucleotides can be used for diagnosis, treatment and prevention of
 CC PTEN-related diseases, e.g. infections, inflammation and tumours.
 CC The present sequence represents the human PTEN protein sequence.
 XX
 XX Sequence 403 AA;
 Query Match 9.5%; Score 490.5; DB 21; Length 403;
 Best Local Similarity 31.3%; Pred. No. 7.2e-33;
 Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
 QY 48 IFTAVSSNRCTEQYQNDLDCAYITDRIIAIGYPATGIEANFRNSKVQTOQLTRRHGK 107
 Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H - K 62
 QY 108 G N V K F N L R G G Y Y D A N D F G N V I C F D M T D H P P S L E M A P F C R E A K E W L E A D D K H V I A V 167
 Db 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q L S E D D N H V A I 122
 QY 168 H C K A G K R T G V M I C A L L I Y I N F P S P R Q I L D Y S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 227
 Db 123 H C K A G K R T G V M I C A L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S O R R Y I Y Y S Y L L 182
 QY 228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E G N G S T I L F K P D P L I I S K S N H Q R E R A 287
 Db 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G ----- T C N P Q F V V C Q L K V I Y S N S G P T R R - 234
 QY 288 T W L N N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I - - R E I G F L K K F S 345
 Db 235 ----- E D K F ----- M Y F E F P Q P L P V C - - G D I K V E F F H K Q N K M L K K - - 267
 QY 346 D G K I G H V W F N T M P ----- A C D G G L N G - G H F E Y V D K T Q P Y I G D D T S I G R K N 389
 Db 268 - D K M F H F W N T F F I P G P E E T S E K V E N G S L C D Q E I D S I C S I E R A D N D K E Y L ----- 316
 QY 390 G M R R N E T P M R K I D P E T G N E F E S P 412
 Db 317 V L T L T K N D L D K A N K A N R Y F S P 339
 Search completed: December 10, 2003, 20:32:16
 Job time : 62.1676 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	508.5	9.8	430	3	US-08-791-1158-7	Sequence 7, Appl
2	508.5	9.8	430	4	US-09-140-749-18	Sequence 18, Appl
3	507.5	9.8	565	3	US-08-906-156A-12	Sequence 12, Appl
4	507	9.8	559	4	US-09-140-749-15	Sequence 15, Appl
5	507	9.8	597	4	US-09-140-749-8	Sequence 8, Appl
6	507	9.8	645	3	US-08-791-1158-6	Sequence 6, Appl
7	507	9.8	742	3	US-08-791-1158-5	Sequence 5, Appl
8	490.5	9.5	394	3	US-08-791-1158-27	Sequence 27, Appl
9	490.5	9.5	394	4	US-09-140-749-17	Sequence 17, Appl
10	490.5	9.5	403	3	US-08-791-1158-1	Sequence 1, Appl
11	490.5	9.5	403	3	US-08-791-1158-23	Sequence 23, Appl
12	490.5	9.5	403	3	US-08-791-1158-25	Sequence 25, Appl
13	490.5	9.5	403	4	US-09-140-749-2	Sequence 2, Appl
14	490.5	9.5	403	4	US-09-140-749-10	Sequence 10, Appl
15	490.5	9.5	403	4	US-09-140-749-49	Sequence 49, Appl
16	490.5	9.5	403	4	US-09-140-749-55	Sequence 55, Appl
17	490.5	9.5	403	4	US-09-140-749-57	Sequence 57, Appl
18	152	2.9	783	6	5231168-2	Sequence 57, Appl
19	137.5	2.7	1177	4	US-09-134-001C-5106	Patent No. 5231168
20	136	2.6	1053	4	US-09-394-272-6	Sequence 5106, Ap
21	133.5	2.6	1054	1	US-08-356-354-4	Sequence 6, Appl
22	133.5	2.6	1054	2	US-08-778-656-4	Sequence 4, Appl
23	130.5	2.5	1054	4	US-09-394-272-3	Sequence 4, Appl
24	130.5	2.5	1852	1	US-08-425-061-24	Sequence 3, Appl
25	130.5	2.5	1852	2	US-08-825-886-24	Sequence 24, Appl
26	130.5	2.5	1852	1	US-08-989-890-24	Sequence 24, Appl
27	130.5	2.5	1863	1	US-08-425-061-16	Sequence 16, Appl

QY 69 CAVITDRITAIAGVPATGIEANERNKSVQOQFLTRHKGKGVNLRGGVYYDADNFDG 128
 Db 61 LTYIYPIIANGPFAERLGGVYNNIDDDVRELDKSH-KNHVKIYNLCARHYDTAKFNC 119
 QY 129 NVICFDMTDHPPSLBELMAFFCREAKWLEADKHVIAVHCAGKAGRTGVMICALLIYN 188
 Db 120 RVAQYFFEDHNPQLELIPFCEDLDWLSEDDNHVAAHCKAGKAGRTGVMICAYLLHRG 179
 QY 189 FVSPRQILDYYSIIRTKNKGVTIPSORRYIYYHKLRLERENYVPLRMQLIGVYVERP 248
 Db 180 KFLKAQEAALDFYGEVTRDKKGVTIIPSORRYIYYHKLRLERENYVPLRMQLIGVYVERP 239
 QY 249 PKTWGGGSKIKEVEGNGSTILFKPDPLIISKNHQRERATWLNCCDTPNEPDTGQKYHG 308
 Db 240 PMFSGG-----TCNPQVVCQLKVKIYSSNSGPTRR-----EDKF-- 274
 QY 309 FVSKRAYCFMVPEDAPVFEVGDVRIDI--REIGFLKFKSDGKIGHVWNTMF----- 358
 Db 275 -----MYFEFQPLPVC--GDIKVEFFHKQKMLKK--DKMFHFWNTTFFIPGPEETS 323
 QY 359 -----ACDGLNG-GHFEYVDKTPYIGDDTSIGRKNGMRRNETPMRKIDPETGNBEF 410
 Db 324 EKVENGSLCDQBIIDSICSTERADNDKEYL-----VLTLTKNLDLKANKKANYF 373
 QY 411 SP 412
 Db 374 SP 375

RESULT 2
 US-09-140-749-18
 ; Sequence 18, Application US/09140749
 ; Patent No. 6482795
 ; GENERAL INFORMATION:
 ; APPLICANT: Steck, Peter
 ; APPLICANT: Pershouse, Mark A.
 ; APPLICANT: Jasser, Samar
 ; APPLICANT: Yung, Alfred W.K.
 ; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
 ; FILE REFERENCE: 2318-205
 ; CURRENT APPLICATION NUMBER: US/09/140,749
 ; EARLIER FILING DATE: 1998-08-26
 ; EARLIER FILING DATE: 1997-01-30
 ; EARLIER FILING DATE: 1997-01-30
 ; EARLIER FILING DATE: 1997-08-26
 ; EARLIER FILING DATE: 1998-04-30
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 18
 ; LENGTH: 430
 ; TYPE: PRT
 ; ORGANISM: Canis familiaris
 US-09-140-749-18

Query Match 9.8%; Score 508.5; DB 4; Length 430;
 Best Local Similarity 30.3%; Pred. No. 1.5e-34;
 Matches 128; Conservative 66; Mismatches 163; Indels 65; Gaps 10;
 QY 9 PSTSTRMARDLOENPNRQGEPRVSEPHVNSIVERIRHIFRTAVSSNCRTEYQNIIDL 68
 Db 1 PPAARPGACSLRRRRPPLPSLSFLSSHLRPLDPTAIKEIVSRNRRRYQEDGFOLD 60
 QY 69 CAVITDRITAIAGVPATGIEANERNKSVQOQFLTRHKGKGVNLRGGVYYDADNFDG 128
 Db 61 LTYIYPIIANGPFAERLGGVYNNIDDDVRELDKSH-KNHVKIYNLCARHYDTAKFNC 119
 QY 129 NVICFDMTDHPPSLBELMAFFCREAKWLEADKHVIAVHCAGKAGRTGVMICALLIYN 188
 Db 120 RVAQYFFEDHNPQLELIPFCEDLDWLSEDDNHVAAHCKAGKAGRTGVMICAYLLHRG 179

QY 189 FVSPRQILDYYSIIRTKNKGVTIPSORRYIYYHKLRLERENYVPLRMQLIGVYVERP 248
 Db 180 KFLKAQEAALDFYGEVTRDKKGVTIIPSORRYIYYHKLRLERENYVPLRMQLIGVYVERP 239
 QY 249 PKTWGGGSKIKEVEGNGSTILFKPDPLIISKNHQRERATWLNCCDTPNEPDTGQKYHG 308
 Db 240 PMFSGG-----TCNPQVVCQLKVKIYSSNSGPTRR-----EDKF-- 274
 QY 309 FVSKRAYCFMVPEDAPVFEVGDVRIDI--REIGFLKFKSDGKIGHVWNTMF----- 358
 Db 275 -----MYFEFQPLPVC--GDIKVEFFHKQKMLKK--DKMFHFWNTTFFIPGPEETS 323
 QY 359 -----ACDGLNG-GHFEYVDKTPYIGDDTSIGRKNGMRRNETPMRKIDPETGNBEF 410
 Db 324 EKVENGSLCDQBIIDSICSTERADNDKEYL-----VLTLTKNLDLKANKKANYF 373
 QY 411 SP 412
 Db 374 SP 375

RESULT 3
 US-08-906-156A-12
 ; Sequence 12, Application US/08906156A
 ; Patent No. 6287854
 ; GENERAL INFORMATION:
 ; APPLICANT: SPURR, NIGEL K
 ; APPLICANT: GRAY, IAN C
 ; APPLICANT: STEWART, LORNA M
 ; TITLE OF INVENTION: DIAGNOSIS OF SUSCEPTIBILITY TO CANCER
 ; TITLE OF INVENTION: AND TREATMENT THEREOF
 ; NUMBER OF SEQUENCES: 94
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P. C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/906,156A
 ; FILING DATE: 05-AUG-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/042,655
 ; FILING DATE: 02-APR-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/033,147
 ; FILING DATE: 13-DEC-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/005,840
 ; FILING DATE: 23-OCT-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/96GB/02588
 ; FILING DATE: 22-OCT-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SADORFF, B.J.
 ; REGISTRATION NUMBER: 36,663
 ; REFERENCE/DOCKET NUMBER: 1090-14
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-816-4000
 ; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 565 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single

```
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Translation of partial cDNA sequence
US-08-906-156A-12

Query Match
Best Local Similarity 9.8%; Score 507.5; DB 3; Length 565;
Matches 130; Conservative 66; Mismatches 159; Indels 61; Gaps 11;

QY 10 STSTRSMARD-LQENPNRQPGPRVSEPHNSIVERIRHIFRTAVSSNRCRTQYQNDLID 68
Db 127 SATAKSRAISILQKKPRHQQLPSLSFFSHRLPDMTAAIKIIVSRNKRKYQEDGFOLD 186

QY 69 CAYITDRIIAIGYPATGIEANFRNSKVQTOQFLTRRHGKGNVKNVFNLRGGYVYDADNFDG 128
Db 187 LTYIYPNIIANGFPAERLEGVYRNNDVVRFLDSKH-KNHYKIYNLCAERHYDTAKFNC 245

QY 129 NVICFDMTHDHPSPLEMAPFCREAKEWLEADKHVIAVHCAGKGRGTGVMICALLIYIN 188
Db 246 RVAQYPPFDHNPQLELIKPFCELDQWLSDDNHVAAIHCKAGKGRGTGVMICAYLLHRG 305

QY 189 FYPSPRQILDYYSIIRTKNKGVTIPSORRYIYYHKLRERELNYLPLRMQLIGVYVERP 248
Db 306 KFLKAQALDFGEVTRDKKGVITPSQRRYIYYSLKKNHLDYRVPALLFHKMFMFTI 365

QY 249 PKTWGGGSKIKVEVNGSGTILFKPDLPIISKSNHORERATWLNCDTNEFDTGQKYHG 308
Db 366 PMFSGG-----TCNPQFVVCQLKVIYSSNSGPTRR-----EDKF-- 400

QY 309 FVSKRAYCFMVPEDAPVFEVDGRIDI--REIGFLKKFSDGKIGHVFWNTMF----- 358
Db 401 -----MYFEFPQPLFVC--GDIKVEFFHKQKNMLKK-----DKMFHFVWNTFPIGPPEETS 449

QY 359 -----ACDGLNG-GHFEYVDKTPYI-----GDDTSIGRKNMGRRNETPMRKI 401
Db 450 EKVENGSLCDQEIIDSICSIERADNDKEYLVLTLTKNDLKDANKKANKRYFSPFKV 505

RESULT 4
US-09-140-749-15
; Sequence 15, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; EARLIER FILING DATE: 1998-08-26
; EARLIER FILING DATE: 1997-01-30
; EARLIER FILING DATE: 1997-08-26
; EARLIER FILING DATE: 1997-08-26
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-140-749-15

Query Match
Best Local Similarity 9.8%; Score 507; DB 4; Length 559;
Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;

QY 10 STSTRSMARD-LQENPNRQPGPRVSEPHNSIVERIRHIFRTAVSSNRCRTQYQNDLID 68
Db 159 SATAKSRAISILQKKPRHQQLPSLSFFSHRLPDMTAAIKIIVSRNKRKYQEDGFOLD 218

QY 69 CAYITDRIIAIGYPATGIEANFRNSKVQTOQFLTRRHGKGNVKNVFNLRGGYVYDADNFDG 128
Db 219 LTYIYPNIIANGFPAERLEGVYRNNDVVRFLDSKH-KNHYKIYNLCAERHYDTAKFNC 277

QY 129 NVICFDMTHDHPSPLEMAPFCREAKEWLEADKHVIAVHCAGKGRGTGVMICALLIYIN 188
Db 246 RVAQYPPFDHNPQLELIKPFCELDQWLSDDNHVAAIHCKAGKGRGTGVMICAYLLHRG 305

Query Match
Best Local Similarity 9.8%; Score 507; DB 4; Length 597;
Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;

QY 10 STSTRSMARD-LQENPNRQPGPRVSEPHNSIVERIRHIFRTAVSSNRCRTQYQNDLID 68
Db 159 SATAKSRAISILQKKPRHQQLPSLSFFSHRLPDMTAAIKIIVSRNKRKYQEDGFOLD 218

QY 69 CAYITDRIIAIGYPATGIEANFRNSKVQTOQFLTRRHGKGNVKNVFNLRGGYVYDADNFDG 128
Db 219 LTYIYPNIIANGFPAERLEGVYRNNDVVRFLDSKH-KNHYKIYNLCAERHYDTAKFNC 277

QY 129 NVICFDMTHDHPSPLEMAPFCREAKEWLEADKHVIAVHCAGKGRGTGVMICALLIYIN 188
Db 246 RVAQYPPFDHNPQLELIKPFCELDQWLSDDNHVAAIHCKAGKGRGTGVMICAYLLHRG 305
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Db 278 RVAQPFEDHNPQLEIKPFCELDQWLSDDHVAIHCAGKRGVWICAYLLHRG 337
Qy 189 FVPSRQLDYYSIIRTKNNKGVTPISQRRYIYYHKLREELNYLPLRMQLIGVYVERP 248
Db 338 KFLKAQEAALDFYGEVTRDKKGVTPISQRRYVYVSYLLKNHLDYRPVALLPHKMPETI 397
Qy 249 PXTWGGGSKIKVEVNGSTILFKPDPDLIISKNHOREATWLNCDTNEFTDGEQKYHG 308
Db 398 PMFSGG-----TCNPQVVCQVKVIYSSNGPTR-----EDKF-- 432
Qy 309 FVSKRAYCFMVPEDAPVFEVDVIRDI--REIGFLKFKSDGKIGHVWENTMF----- 358
Db 433 -----MYFEPQPLPVC--GDIKVEFFHKQNMKK--DKMFHFWNTTFIPGPEETS 481
Qy 359 -----ACDGLNG-GHFEYVDKTPYIGDDTSIGRKNMRRNETPMRKIDPETGNEFE 410
Db 482 EKVENGLCDQEBIDSICSIERADNDKEYL-----VLTLTCKNDLCKANKDKANRYF 531
Qy 411 SP 412
Db 532 SP 533

RESULT 6
US-08-791-115B-6
; Sequence 6, Application US/08791115B
; Patent No. 6262242
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, W.K. Alfred
; APPLICANT: Tavtigan, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,115B
; FILING DATE: 30-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 38,957
; REFERENCE/DOCKET NUMBER: 2318-134.A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-683-6040
; TELEFAX: 202-683-7031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 645 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-791-115B-6
Query Match 9.8%; Score 507; DB 3; Length 645;
Best Local Similarity 30.6%; Pred. No. 3.8e-34;
Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;
Qy 10 STSTRSMARD-LQENPNRQGEPRVSEPHVNSIVERIHFRTAVSSNRCRTEYQIDLD 68

Db 207 SATAKSRAISLQKKPRHQQLPSLSFFFSHRLPDMTALIKETVSRNKRRYQEDGFELD 266
Qy 69 CAYITDRIIAGYATGIEANFRNSKVOTQOFLTRRHGKGNVKNVFNLRGGYVYADNFDG 128
Db 267 LTYIYPNIIAMGFFPAERLEGVYRNIDDDVRFLLSKH-KNHYKIYNLCAERHYDTAKFNC 325
Qy 129 NVICFDMTDHPPSSLEMAPECREAKWLEADDKHVIAVHCAGKRGVWICALLIYIN 188
Db 326 RVAQPFEDHNPQLEIKPFCELDQWLSDDHVAIHCAGKRGVWICAYLLHRG 385
Qy 189 FVPSRQLDYYSIIRTKNNKGVTPISQRRYIYYHKLREELNYLPLRMQLIGVYVERP 248
Db 386 KFLKAQEAALDFYGEVTRDKKGVTPISQRRYVYVSYLLKNHLDYRPVALLPHKMPETI 445
Qy 249 PXTWGGGSKIKVEVNGSTILFKPDPDLIISKNHOREATWLNCDTNEFTDGEQKYHG 308
Db 446 PMFSGG-----TCNPQVVCQVKVIYSSNGPTR-----EDKF-- 480
Qy 309 FVSKRAYCFMVPEDAPVFEVDVIRDI--REIGFLKFKSDGKIGHVWENTMF----- 358
Db 481 -----MYFEPQPLPVC--GDIKVEFFHKQNMKK--DKMFHFWNTTFIPGPEETS 529
Qy 359 -----ACDGLNG-GHFEYVDKTPYIGDDTSIGRKNMRRNETPMRKIDPETGNEFE 410
Db 530 EKVENGLCDQEBIDSICSIERADNDKEYL-----VLTLTCKNDLCKANKDKANRYF 579
Qy 411 SP 412
Db 580 SP 581

RESULT 7
US-08-791-115B-5
; Sequence 5, Application US/08791115B
; Patent No. 6262242
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, W.K. Alfred
; APPLICANT: Tavtigan, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,115B
; FILING DATE: 30-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 38,957
; REFERENCE/DOCKET NUMBER: 2318-134.A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-683-6040
; TELEFAX: 202-683-7031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 742 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-791-115B-5

Query Match 9.8%; Score 507; DB 3; Length 742;
Best Local Similarity 30.6%; Pred. No. 4.8e-34;
Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;
QY 10 STSTESMAED-LOENPNQPGEPVSEPHNSIVERIRHIFRTAVSSNRCRTEYQNIIDL 68
DB 304 SATAKSRAISILOKPRHQQLPSLSFFSHRLPDMTAIKEIIVSRNKRKYQEDGFDLD 363
QY 69 CAYITDRIIAGYPATGIEANFRNSKVQOQFLTRRHGKGNVFNLRGGVYVDADNFDG 128
DB 364 LTYIYPNIIAMGFPARLEGVYRNIDDVVRLDSKH-KHYKIYNLCARHYDTAKENC 422
QY 129 NVICFDMTHHPPSLELMAPPCEAKEMLEADKHVIAVHCAGKRGRTGVMICALLIYN 188
DB 423 RVAQYPPFEDHNPQLELIKPFCEDLQMLSEDDNHVAATHCAGKRGRTGVMICAYLLHRG 482
QY 189 FYPSPQILDYYSIIRTKNNKGVTPISORRYIYVYHKLREELNLYPLRMQLIGVYVERP 248
DB 483 KFLKAQALDFYGEVTRDKKGVTPISORRYIYVYHKLREELNLYPLRMQLIGVYVERP 542
QY 249 PKTWGGGSKIKVEVNGSTILFKPDPLIISKSNHORERATWLNNDCTPNEFDTGQKYHG 308
DB 543 PMFSGG-----TCNPQFVVCQKVIYSSNSGPTRR-----EDKF-- 577
QY 309 FVSKRAYCPMVPEDAPVFEVDVRI--REIGFLKFSGDKIGHVWNTMF----- 358
DB 578 -----MYFEFPQPLPVC--GDIKVEFFHKQKMLKK--DKMFHFVWNTFPFGPEETS 626
QY 359 -----ACDGLNG-GHPEYVDKTPYIGDDTSIGRKNMRNTPMRKIDPETGNEFE 410
DB 627 EKVENGLSCQDEISCSIERADNDKEYL-----VLTITKNDLDRKANKKANYF 676
QY 411 SP 412
DB 677 SP 678
RESULT 8
US-08-791-115B-27
; Sequence 27, Application US/08791115B
; Patent No. 626242
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, W.K. Alfred
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: Rothwell, Figg, Earnst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,115B
; FILING DATE: 30-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 38,957
; REFERENCE/DOCKET NUMBER: 2318-134.A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-683-6040
; TELEFAX: 202-683-7031

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-115B-27

Query Match 9.5%; Score 490.5; DB 3; Length 394;
Best Local Similarity 31.3%; Pred. No. 4.4e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
QY 48 IFRFVSSNRRTYQNIIDLCAVITRIIAGYPATGIEANFRNSKVQOQFLTRRHGK 107
DB 4 IIKIVSRNKRKYQEDGFDLDLTYIYPNIIAMGFPARLEGVYRNIDDVVRLDSKH-K 62
QY 108 GNVFENLRGGVYVDADNFDGVCFTMDTHHPPSLELMAPPCEAKEMLEADKHVIAV 167
DB 63 NHYKIYNLCARHYDTAKFNCVQAQYFEDHNPQLELIKPFCEDLQMLSEDDNHVAI 122
QY 168 HCKAGKRGRTGVMICALLIYNFYPSPQILDYYSIIRTKNNKGVTPISORRYIYVYHKL 227
DB 123 HCKAGKRGRTGVMICAYLLHRGKFLKAQALDFYGEVTRDKKGVTPISORRYIYVYHKL 182
QY 228 ERELNLYPLRMQLIGVYVERPPTKWTGGGSKIKVEVNGSTILFKPDPLIISKSNHORERA 287
DB 183 KNLHDYRPVALLFHKMPETIEMFSGG-----TCNPQFVVCQKVIYSSNSGPTRR- 234
QY 288 TWLNNDCTPNEFDTGQKYHGFVSKRAYCFMVPEDAPVFEVDVRI--REIGFLKFS 345
DB 235 -----EDKF-----MYFEFPQPLPVC--GDIKVEFFHKQKMLKK-- 267
QY 346 DGKIGHVWNTMF-----ACDGLNG-GHPEYVDKTPYIGDDTSIGRKN 389
DB 268 -DKMFHFVWNTFPFGPEETSEKVENGLSCQDEISCSIERADNDKEYL----- 316
QY 390 GMRNETPMRKIDPETGNEFESP 412
DB 317 VLTITKNDLDRKANKKANYFSP 339

RESULT 9

US-09-140-749-17
; Sequence 17, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 17
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-140-749-17

Query Match 9.5%; Score 490.5; DB 4; Length 394;
Best Local Similarity 31.3%; Pred. No. 4.4e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

US-08-791-115B-23

Query Match 9.5%; Score 490.5; DB 3; Length 403;
Best Local Similarity 31.3%; Pred. No. 4.6e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRVAVSSNRCTEYQNDLDCAYITDRIIAIGYPATGIEANFRNSKVQTOQFLTRRHGK 107
DB 4 I I K E I V S R N K R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H - K 62

QY 108 GNVKFNLRGGYVDADNFDGNVICFDMTDHHPSPSLELMAPFCREAKEWLEADDKHVIAV 167
DB 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E L I K P C E D L D Q W L S E D D N H V A I 122

QY 168 HCKAGKGRGTGMICALLIYINFPSPRQILDYYSIIRTKNNKGVTPSQRRYIYYHKL 227
DB 123 HCKAGKGRGTGMICAYLLHRGKFLKAQEALEDYFGEVTRDKKGVTPSQRRYIYYHKL 182

QY 228 ERELNYLPLRMOLIGYVVERPPTKWWGGSKIKVEVNGSTILFKPDPPLIISKSNHQRERA 287
DB 183 K N H L D Y R P V A L L F H K M P E T I P M F S G G - - - - - T C N P Q V V C L K V K I Y S N S G P T R R - 234

QY 288 T W L N C D T N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I - - R E I G F L K K F S 345
DB 235 - - - - - E D K F - - - - - M Y F E P Q P L P V C - - G D I K V E F F H K N K M L K - - 267

QY 346 D G K I G H V W F N T M F - - - - - A C D G L N G - G H F E Y V D K T Q P Y I G D D T S I G R K N 389
DB 268 - D K M F H F W N T F I P G P E T S E K V E N G S L C D Q E I D S I E R A D N D K E Y L - - - - - 316

QY 390 G M R N E T P M R K I D P E T G N E F S P 412
DB 317 V L T L T K N D L D K A N K D K A N R Y F S P 339

RESULT 12

US-08-791-115B-25
Sequence 25, Application US/08791115B
Patent No. 6262242
GENERAL INFORMATION:
APPLICANT: Steck, Peter
APPLICANT: Pershouse, Mark A.
APPLICANT: Jasser, Samar
APPLICANT: Yung, W.K. Alfred
APPLICANT: Tavtighian, Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,115B
FILING DATE: 30-JAN-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 38,957
REFERENCE/DOCKET NUMBER: 2318-134.A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-683-6040
TELEFAX: 202-683-7031
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-115B-25

Query Match 9.5%; Score 490.5; DB 3; Length 403;
Best Local Similarity 31.3%; Pred. No. 4.6e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRVAVSSNRCTEYQNDLDCAYITDRIIAIGYPATGIEANFRNSKVQTOQFLTRRHGK 107
DB 4 I I K E I V S R N K R Y Q E D G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N N I D D V V R F L D S K H - K 62

QY 108 GNVKFNLRGGYVDADNFDGNVICFDMTDHHPSPSLELMAPFCREAKEWLEADDKHVIAV 167
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DB 183 K N H L D Y R P V A L L F H K M P E T I P M F S G G - - - - - T C N P Q V V C L K V K I Y S N S G P T R R - 234

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DB 235 - - - - - E D K F - - - - - M Y F E P Q P L P V C - - G D I K V E F F H K N K M L K - - 267

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DB 317 V L T L T K N D L D K A N K D K A N R Y F S P 339

RESULT 13

US-09-140-749-2
Sequence 2, Application US/09140749
Patent No. 6482795
GENERAL INFORMATION:
APPLICANT: Steck, Peter
APPLICANT: Pershouse, Mark A.
APPLICANT: Jasser, Samar
APPLICANT: Yung, Alfred W.K.
APPLICANT: Tavtighian, Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
FILE REFERENCE: 2318-205
CURRENT APPLICATION NUMBER: US/09/140,749
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: U.S. 08/791,115
EARLIER FILING DATE: 1997-01-30
EARLIER APPLICATION NUMBER: U.S. 60/057,750
EARLIER FILING DATE: 1997-08-26
EARLIER APPLICATION NUMBER: U.S. 60/083,563
EARLIER FILING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 2
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-09-140-749-2

Query Match 9.5%; Score 490.5; DB 4; Length 403;
Best Local Similarity 31.3%; Pred. No. 4.6e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRVAVSSNRCTEYQNDLDCAYITDRIIAIGYPATGIEANFRNSKVQTOQFLTRRHGK 107
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RESULT 14
US-09-140-749-10
; Sequence 10, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-140-749-10

Query Match 9.5%; Score 490.5; DB 4; Length 403;
Best Local Similarity 31.3%; Pred. No. 4.6e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFTAVSSNRCRTEYQNIDLCAVITDRIIAGYPATGIEANFRNSKVQTOQLTRRHGK 107
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RESULT 15
US-09-140-749-49
; Sequence 49, Application US/09140749
; Patent No. 6482795
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-205
; CURRENT APPLICATION NUMBER: US/09/140,749
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: U.S. 08/791,115
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: U.S. 60/057,750
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: U.S. 60/083,563
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-140-749-49

Query Match 9.5%; Score 490.5; DB 4; Length 403;
Best Local Similarity 31.3%; Pred. No. 4.6e-33;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFTAVSSNRCRTEYQNIDLCAVITDRIIAGYPATGIEANFRNSKVQTOQLTRRHGK 107
Db 4 IIEIVSRNKRKYQEDGFDLDLYIYPNIANGFPAERLEGVYRNNDVVRFLDSKH-K 62

QY 108 GNVKFNLRGGYYADNFDGNCVCFDMDTHPPSLELMAPCFREAKEWLEADDKHVIAT 167
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Job time : 24.8315 secs

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GenCore version 5.1.6
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Run on: December 10, 2003, 20:34:18 ; Search time 42.9968 Seconds
(without alignments)
4170.856 Million cell updates/sec

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Perfect score: 5168
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5168	100.0	962	12 US-09-963-693-310	Sequence 310, App
3	1330	25.7	248	9 US-09-205-658-308	Sequence 308, App
4	1330	25.7	248	12 US-09-963-693-308	Sequence 308, App
5	508.5	9.8	430	12 US-10-299-003-18	Sequence 18, Appl
6	507	9.8	559	12 US-10-299-003-15	Sequence 15, Appl
7	507	9.8	597	12 US-10-299-003-8	Sequence 8, Appl
8	490.5	9.5	394	12 US-10-299-003-17	Sequence 17, Appl
9	490.5	9.5	403	10 US-09-870-379-2	Sequence 2, Appli
10	490.5	9.5	403	12 US-10-299-003-2	Sequence 2, Appli
11	490.5	9.5	403	12 US-10-299-003-10	Sequence 10, Appl
12	490.5	9.5	403	12 US-10-299-003-49	Sequence 49, Appl
13	490.5	9.5	403	12 US-10-299-003-55	Sequence 55, Appl
14	490.5	9.5	403	12 US-10-299-003-57	Sequence 57, Appl
15	490.5	9.5	403	15 US-10-059-585-50	Sequence 50, Appl

16	465	9.0	249	9 US-09-205-658-309	Sequence 309, App
17	465	9.0	249	12 US-09-963-693-309	Sequence 309, App
18	368	7.1	445	12 US-10-120-801-99	Sequence 99, Appl
19	342	6.6	645	12 US-10-120-801-101	Sequence 101, App
20	342	6.6	664	12 US-10-120-801-100	Sequence 100, App
21	333.5	6.5	551	12 US-10-120-801-97	Sequence 97, Appl
22	333.5	6.5	551	12 US-10-120-801-98	Sequence 98, Appl
23	333.5	6.5	551	15 US-10-059-585-57	Sequence 57, Appl
24	321	6.2	477	12 US-10-120-801-30	Sequence 30, Appl
25	236	4.6	85	9 US-09-864-761-37705	Sequence 37705, A
26	236	4.6	86	12 US-10-029-386-30662	Sequence 30662, A
27	213	4.1	1386	12 US-10-327-414-2	Sequence 2, Appli
28	210	4.1	382	12 US-10-327-414-4	Sequence 4, Appli
29	206	4.0	1300	12 US-10-102-549-2	Sequence 2, Appli
30	206	4.0	1311	12 US-10-354-358-68	Sequence 68, Appl
31	153.5	3.0	862	12 US-10-339-782-492	Sequence 492, App
32	153.5	3.0	910	15 US-10-177-293-449	Sequence 449, App
33	150	2.9	1369	9 US-09-729-674-42	Sequence 42, Appl
34	136	2.6	991	9 US-09-815-242-5803	Sequence 5803, Ap
35	136	2.6	1053	15 US-10-217-700-6	Sequence 6, Appli
36	135.5	2.6	543	12 US-10-032-585-7649	Sequence 7649, Ap
37	135	2.6	1884	10 US-09-785-770A-17	Sequence 17, Appl
38	135	2.6	1907	10 US-09-785-770A-16	Sequence 16, Appl
39	133.5	2.6	1054	9 US-09-376-045-4	Sequence 4, Appli
40	130.5	2.5	980	9 US-09-888-615-65	Sequence 65, Appl
41	130.5	2.5	1054	15 US-10-217-700-3	Sequence 3, Appli
42	126.5	2.4	1616	11 US-09-820-843A-16	Sequence 16, Appl
43	126.5	2.4	1863	10 US-09-734-672-4	Sequence 4, Appli
44	126.5	2.4	1863	11 US-09-982-828-6	Sequence 6, Appli
45	126	2.4	745	12 US-10-032-585-7860	Sequence 7860, Ap

ALIGNMENTS

RESULT 1

US-09-205-658-310
; Sequence 310, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 962
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-310

Query Match	100.0%	Score 5168;	DB 9;	Length 962;
Best Local Similarity	100.0%;	Pred. No. 0;		
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181 CALLIYINFPSPQRIIDYYSIIRTKNNKGVITPSQRRYIYYHKLRERELNYLPLRMQL 240
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US-09-963-693-310
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; APPLICANT: Ruvkun, Gary
; APPLICANT: Osg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963,693
; CURRENT FILING DATE: 2001-09-25

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; PRIOR APPLICATION NUMBER: US/09/205,658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/857,076
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: 08/888,534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US98/10080
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 962
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-963-693-310

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Query Match 100.0%; Score 5168; DB 12; Length 962;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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301 TGEQKHGFSKRAYCFMVPEDAPVFEVDVIRIDIREIGFLKFSKGKIGHVWNTMFAC 360
361 DGLNGGHFEYVDKTPYIGDDTSIGRKNGMRRNETPMRKIDPETGNEFESPMQIVNPPG 420
361 DGLNGGHFEYVDKTPYIGDDTSIGRKNGMRRNETPMRKIDPETGNEFESPMQIVNPPG 420
421 LEKHITTEQAMENYTNMGIMPPRYTISKILHEKHEKGIKVDYNDNRKLPMDGKSYTESGK 480
421 LEKHITTEQAMENYTNMGIMPPRYTISKILHEKHEKGIKVDYNDNRKLPMDGKSYTESGK 480
481 SGDIRGVGGPFEIPYKABEHLVTFPVYEMDRALKSKDLNNGMKLHVLRVCDTRDSKME 540
481 SGDIRGVGGPFEIPYKABEHLVTFPVYEMDRALKSKDLNNGMKLHVLRVCDTRDSKME 540
541 KSEVFGNLAFFHNESTRRLQALQTMNPKWRPEPCAFGSKGAEMHYPPSVRYSSNDGKYNGA 600
541 KSEVFGNLAFFHNESTRRLQALQTMNPKWRPEPCAFGSKGAEMHYPPSVRYSSNDGKYNGA 600
601 CSENLVSDFFEHNRNIAVLNRYCRYFYKQSTSRSRYPKFRYCPILKKGFIYPADTDDVD 660
601 CSENLVSDFFEHNRNIAVLNRYCRYFYKQSTSRSRYPKFRYCPILKKGFIYPADTDDVD 660
661 ENGQPFHSPHYIKEQEKIDAEKAKGIENGTGPGSTSGSSAPGTIKKTEASQSKVKPAT 720
661 ENGQPFHSPHYIKEQEKIDAEKAKGIENGTGPGSTSGSSAPGTIKKTEASQSKVKPAT 720
721 EDELPPARLPDNRVRRFPVGVDFENPEESCEHKTVESIAGFEPLEHLFHSYHPNTAGN 780
721 EDELPPARLPDNRVRRFPVGVDFENPEESCEHKTVESIAGFEPLEHLFHSYHPNTAGN 780
781 MLRQDYHTDSEVKIAEQEAKAFVDQLNGQGVLFQEFMKQFVPSDNSFADYVVGQAEVFK 840

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Db 781 MLRQYHDTSEVKIAEQEAKAFVDQLLNGGVQLQFMKQFVPSNSFADYVITGQAEVFK 840
QY 841 AQIALLESQEDQRYOANAEVDLEHTLGEAFERFCHVVEESNGSKNPKALKTRQOMVK 900
Db 841 AQIALLESQEDQRYOANAEVDLEHTLGEAFERFCHVVEESNGSKNPKALKTRQOMVK 900
QY 901 ETGKDTQKTRNHLVLEHLEANHRVQIERRETCTELHPEDKIPRIAHFSENSFSDSNFDOAI 960
Db 901 ETGKDTQKTRNHLVLEHLEANHRVQIERRETCTELHPEDKIPRIAHFSENSFSDSNFDOAI 960
QY 961 YL 962
Db 961 YL 962

RESULT 3
US-09-205-658-308
; Sequence 308, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-658-308

Query Match 25.7%; Score 1330; DB 9; Length 248;
Best Local Similarity 99.2%; Pred. No. 2.3e-98;
Matches 246; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 IFRVAVSSNRCRTEYQNIIDLCAYITDRIIAGYPATGIEANFRNSKVQTOQFLTRRHGK 107
Db 1 IFRVAVSSNRCRTEYQNIIDLCAYITDRIIAGYPATGIEANFRNSKVQTOQFLTRRHGK 60
QY 108 GNVKFNLRGGYYDADNFDGNVICFDMTDHHPSPSLELMAPFCREAKEWLEADDKHVIIV 167
Db 61 GNVKFNLRGGYYDADNFDGNVICFDMTDHHPSPSLELMAPFCREAKEWLEADDKHVIIV 120
QY 168 HCKAGKGRGTVMICALLYINFPSPROILDYYSITRTKNNKGVITIPSORRYIYYHKL 227
Db 121 HCKAGKGRGTVMICALLYINFPSPROILDYYSITRTKNNKGVITIPSORRYIYYHKL 180
QY 228 ERELNYPLRMQLIGVYVERPPTKWTGGGSKIKVEYNGSTILFKPDPPLIISKSNHQRERA 287
Db 181 ERELNYPLRMQLIGVYVERPPTKWTGGGSKIKVEYNGSTILFKPDPPLIISKSNHQRERA 240
QY 288 TWLNACDT 295
Db 241 TWLNACDT 248

RESULT 4
US-09-963-693-308
; Sequence 308, Application US/09963693
; Publication No. US20030181364A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary

; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963,693
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/205,658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/857,076
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: 08/888,534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US98/10080
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-693-308

Query Match 25.7%; Score 1330; DB 12; Length 248;
Best Local Similarity 99.2%; Pred. No. 2.3e-98;
Matches 246; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 IFRVAVSSNRCRTEYQNIIDLCAYITDRIIAGYPATGIEANFRNSKVQTOQFLTRRHGK 107
Db 1 IFRVAVSSNRCRTEYQNIIDLCAYITDRIIAGYPATGIEANFRNSKVQTOQFLTRRHGK 60
QY 108 GNVKFNLRGGYYDADNFDGNVICFDMTDHHPSPSLELMAPFCREAKEWLEADDKHVIIV 167
Db 61 GNVKFNLRGGYYDADNFDGNVICFDMTDHHPSPSLELMAPFCREAKEWLEADDKHVIIV 120
QY 168 HCKAGKGRGTVMICALLYINFPSPROILDYYSITRTKNNKGVITIPSORRYIYYHKL 227
Db 121 HCKAGKGRGTVMICALLYINFPSPROILDYYSITRTKNNKGVITIPSORRYIYYHKL 180
QY 228 ERELNYPLRMQLIGVYVERPPTKWTGGGSKIKVEYNGSTILFKPDPPLIISKSNHQRERA 287
Db 181 ERELNYPLRMQLIGVYVERPPTKWTGGGSKIKVEYNGSTILFKPDPPLIISKSNHQRERA 240
QY 288 TWLNACDT 295
Db 241 TWLNACDT 248

RESULT 5
US-10-299-003-18
; Sequence 18, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigan, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 430

; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-299-003-18

Query Match 9.8%; Score 508.5; DB 12; Length 430;
Best Local Similarity 30.3%; Pred. No. 3.8e-32;
Matches 128; Conservative 66; Mismatches 163; Indels 65; Gaps 10;

QY 9 PSTSTRMARDLOENPNRQGPVSEPYHNSIVIRHIFRTAVSSNRCRTEYQNIIDL 68
DB 1 PPAARFGAACSRRRPRRPLPSLSFLSSFLSHRLPDMTAAIKIIVSRNKRKYQEDGFDLD 60
QY 69 CAYITDRIITAIGVPATGIEANFRNSKVQOQLTRRHGKGNVKNLRCGGVYDADNFDG 128
DB 61 LTYIYPNIIAMGFFPAERLEGVTRNNIDVVRFLDSKH-KNHYKIYNLCARHYDTAKFNC 119
QY 129 NVICFDMTDHPPSLELMAPFCREAKEWLEADDDKHVIAVHCKAGKGRGTGMICALLIYN 188
DB 120 RVAQYFFEDHNPQLELIKPFCELDQWLSDDNHVAIHCAGKGRGTGMICAYLLHRG 179
QY 189 FYPSPRQILDYYSIIRTKNKGVTIPSORRYIYYHKLREELNLYPLRMQLIGVYVERP 248
DB 180 KFLKAQEAALDFYGEVTRDKGVTIPSORRYIYYHKLREELNLYPLRMQLIGVYVERP 248
QY 249 PXTWGGGSKIKEVNGSGTILFKPDPLIISKSQHQRERATWLNCDTNEPDTGQKYHG 308
DB 240 PMFSGG-----TCNPQFVVCQKVKIYSSNGPTRR-----EDKF-- 274
QY 309 FVSKRAYCFMVPEDAPVFEVDGVRIDI--REIGFLKFSKDGKIGHVWFTMTF----- 358
DB 275 -----MYFEFPQPLPVC--GDIKVEFFHKQNKMLK---DKMFHFVWNTFFIPGPEETS 323
QY 359 -----ACDGLGNG-GHFEYVDKTPQYIGDDTSIGRKNMGMRNETPMRKIDPETGNEFE 410
DB 324 EKVENGLSDQEIISCSIERADNDKEYL-----VLTITKNDLCKANKKANKRYF 373
QY 411 SP 412
DB 374 SP 375

RESULT 6
US-10-299-003-15
; Sequence 15, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-299-003-15

Query Match 9.8%; Score 507; DB 12; Length 559;
Best Local Similarity 30.6%; Pred. No. 7.6e-32;
Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;

QY 10 STSTRMARDLOENPNRQGPVSEPYHNSIVIRHIFRTAVSSNRCRTEYQNIIDL 68
DB 159 SAKAKSRAISILQKKPRHQQLPSLSFFSHRLPDMTAAIKIIVSRNKRKYQEDGFDLD 218

Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;
QY 10 STSTRMARDLOENPNRQGPVSEPYHNSIVIRHIFRTAVSSNRCRTEYQNIIDL 68
DB 121 SAKAKSRAISILQKKPRHQQLPSLSFFSHRLPDMTAAIKIIVSRNKRKYQEDGFDLD 180
QY 69 CAYITDRIITAIGVPATGIEANFRNSKVQOQLTRRHGKGNVKNLRCGGVYDADNFDG 128
DB 181 LTYIYPNIIAMGFFPAERLEGVTRNNIDVVRFLDSKH-KNHYKIYNLCARHYDTAKFNC 239
QY 129 NVICFDMTDHPPSLELMAPFCREAKEWLEADDDKHVIAVHCKAGKGRGTGMICALLIYN 188
DB 240 RVAQYFFEDHNPQLELIKPFCELDQWLSDDNHVAIHCAGKGRGTGMICAYLLHRG 299
QY 189 FYPSPRQILDYYSIIRTKNKGVTIPSORRYIYYHKLREELNLYPLRMQLIGVYVERP 248
DB 300 KFLKAQEAALDFYGEVTRDKGVTIPSORRYIYYHKLREELNLYPLRMQLIGVYVERP 359
QY 249 PXTWGGGSKIKEVNGSGTILFKPDPLIISKSQHQRERATWLNCDTNEPDTGQKYHG 308
DB 360 PMFSGG-----TCNPQFVVCQKVKIYSSNGPTRR-----EDKF-- 394
QY 309 FVSKRAYCFMVPEDAPVFEVDGVRIDI--REIGFLKFSKDGKIGHVWFTMTF----- 358
DB 395 -----MYFEFPQPLPVC--GDIKVEFFHKQNKMLK---DKMFHFVWNTFFIPGPEETS 443
QY 359 -----ACDGLGNG-GHFEYVDKTPQYIGDDTSIGRKNMGMRNETPMRKIDPETGNEFE 410
DB 444 EKVENGLSDQEIISCSIERADNDKEYL-----VLTITKNDLCKANKKANKRYF 493
QY 411 SP 412
DB 494 SP 495

RESULT 7
US-10-299-003-8
; Sequence 8, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-299-003-8

Query Match 9.8%; Score 507; DB 12; Length 597;
Best Local Similarity 30.6%; Pred. No. 8.4e-32;
Matches 129; Conservative 68; Mismatches 159; Indels 66; Gaps 11;

QY 10 STSTRMARDLOENPNRQGPVSEPYHNSIVIRHIFRTAVSSNRCRTEYQNIIDL 68
DB 159 SAKAKSRAISILQKKPRHQQLPSLSFFSHRLPDMTAAIKIIVSRNKRKYQEDGFDLD 218

QY 69 CAYITDRIIAGPATGIEANFRNSKVQTOQFLTRRHGKGNVFNLRGGYVYDADNPDG 128
 Db 219 LTYIYVNIAMGPAERLEGVYRNNDVVRFLDSKH-KHYKIYNLCAERHYDTAKENC 277
 QY 129 NVICDMTDDHPPSLEMAPFCEKAEWLEADKHVIAVHCAGKGRGTGVMICALLIYN 188
 Db 278 RVAQYFFEDHNPQLELIKPFCELDLWSEDDNHVAIHCAGKGRGTGVMICALLHRG 337
 QY 189 FVPSRQILDYYSIIRTKNKGVTIPSORRYIYYHKLREELNLYPLRMQLIGYVVERP 248
 Db 338 KELKAQEAALDFGEVTRDKGVTIPSORRYVYVYVYLLKNHLDYRVPALLPHKWMFETI 397
 QY 249 PXTWGGSKIKVEVNGSTILFKPDPPLIISKNHQERATWLNCDTNEPTGTQKQVHG 308
 Db 398 PMFSGG-----TCNPQVVCQKVKIYSSNSGPTRR-----EDKF-- 432
 QY 309 FVSKRAYCFMVPEDAPVFEVGVDRIDI--REIGFLKKFSDGKIGHVWNTMF----- 358
 Db 433 -----MYFEFPQPLPVC--GDIKVEFFHKQNMKLLK--DKMFHFWNTFFIPGPEETS 481
 QY 359 -----ACDGLGNG-GHFEYVVDKTPYIGDDTSIGRKNMRRNETPMRKIDPETGNEFE 410
 Db 482 EXVNGSLCQOEIDSICTERADNDKEYL-----VLTLTKNLDLKDANKKANKRYF 531
 QY 411 SP 412
 Db 532 SP 533

RESULT 8
 US-10-299-003-17
 ; Sequence 17, Application US/10299003
 ; Publication No. US20030139324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steck, Peter
 ; APPLICANT: Pershouse, Mark A.
 ; APPLICANT: Jasser, Sanar
 ; APPLICANT: Yung, Alfred W.K.
 ; APPLICANT: Tavtighian, Sean V.
 ; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
 ; FILE REFERENCE: 2318-385
 ; CURRENT APPLICATION NUMBER: US/10/299,003
 ; CURRENT FILING DATE: 2002-11-19
 ; PRIOR APPLICATION NUMBER: U.S. 09/140,749
 ; PRIOR FILING DATE: 1998-08-26
 ; PRIOR FILING DATE: 1997-01-30
 ; PRIOR FILING DATE: 1997-01-30
 ; PRIOR FILING DATE: 1997-08-26
 ; PRIOR FILING DATE: 1998-04-30
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 17
 ; LENGTH: 394
 ; TYPE: PRT
 ; ORGANISM: Canis familiaris
 US-10-299-003-17

Query Match 9.5%; Score 490.5; DB 12; Length 394;
 Best Local Similarity 31.3%; Pred. No. 9.3e-31;
 Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
 QY 48 IFRTAVSSNRCTEYQNIIDLCAYITDRIIAGPATGIEANFRNSKVQTOQFLTRRHGK 107
 Db 4 IIKEIVSRNKRKYQEDGFDLDTIYIPNIAMGPAERLEGVYRNNDVVRFLDSKH-K 62
 QY 108 GNVKFNLRGGYVYDADNPDGVICFDMTHHPPSLEMAPFCEKAEWLEADKHVIAV 167
 Db 63 NHYKIYNLCAERHYDTAKENCRAVQYPPEDHNPQLELIKPFCELDLWSEDDNHVAI 122
 QY 168 HCKAGKGRGTGVMICALLIYNIFPSPROILDYYSIIRTKNKGVTIPSORRYIYYHKL 227

Db 123 HCKAGKGRGTGVMICALLHRGKFLKAQEAALDFGEVTRDKKGVTPISORRYVYVYVYLL 182
 QY 228 ERELNYLPLRMQLIGVYVVERPDKTWGGGSKIKVEVNGSTILFKPDPPLIISKNHQBRRA 287
 Db 183 KNHLDYRVPALLPHKWMFETIPMFSGG-----TCNPQVVCQKVKIYSSNSGPTRR- 234
 QY 288 TWLNCDTNEPTGTQKQVHGFSKRAYCFMVPEDAPVFEVGVDRIDI--REIGFLKKFS 345
 Db 235 -----EDKF-----MYFEFPQPLPVC--GDIKVEFFHKQNMKLLK-- 267
 QY 346 DGKIGHVWNTMF-----ACDGLGNG-GHFEYVVDKTPYIGDDTSIGRKN 389
 Db 268 -DKMFHFWNTFFIPGPEETSEKVENGLCQOEIDSICTERADNDKEYL----- 316
 QY 390 GMRNETPMRKIDPETGNEFESP 412
 Db 317 VLTLTKNLDLKDANKKANKRYFSP 339

RESULT 9
 US-09-870-379-2
 ; Sequence 2, Application US/09870379
 ; Patent No. US20020150954A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donald L. Durden
 ; APPLICANT: ADVANCED RESEARCH & TECHNOLOGY INSTITUTE
 ; TITLE OF INVENTION: Compositions and Methods for Identifying
 ; TITLE OF INVENTION: Agents Which Modulate PTEN Function and PI-3 Kinase Pathways
 ; FILE REFERENCE: ARTI 0024-US
 ; CURRENT APPLICATION NUMBER: US/09/870,379
 ; CURRENT FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/17358
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: 60/274/167
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: 60/208,437
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-870-379-2

Query Match 9.5%; Score 490.5; DB 10; Length 403;
 Best Local Similarity 31.3%; Pred. No. 9.6e-31;
 Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
 QY 48 IFRTAVSSNRCTEYQNIIDLCAYITDRIIAGPATGIEANFRNSKVQTOQFLTRRHGK 107
 Db 4 IIKEIVSRNKRKYQEDGFDLDTIYIPNIAMGPAERLEGVYRNNDVVRFLDSKH-K 62
 QY 108 GNVKFNLRGGYVYDADNPDGVICFDMTHHPPSLEMAPFCEKAEWLEADKHVIAV 167
 Db 63 NHYKIYNLCAERHYDTAKENCRAVQYPPEDHNPQLELIKPFCELDLWSEDDNHVAI 122
 QY 168 HCKAGKGRGTGVMICALLIYNIFPSPROILDYYSIIRTKNKGVTIPSORRYIYYHKL 227
 Db 123 HCKAGKGRGTGVMICALLHRGKFLKAQEAALDFGEVTRDKKGVTPISORRYVYVYVYLL 182
 QY 228 ERELNYLPLRMQLIGVYVVERPDKTWGGGSKIKVEVNGSTILFKPDPPLIISKNHQBRRA 287
 Db 183 KNHLDYRVPALLPHKWMFETIPMFSGG-----TCNPQVVCQKVKIYSSNSGPTRR- 234
 QY 288 TWLNCDTNEPTGTQKQVHGFSKRAYCFMVPEDAPVFEVGVDRIDI--REIGFLKKFS 345
 Db 235 -----EDKF-----MYFEFPQPLPVC--GDIKVEFFHKQNMKLLK-- 267
 QY 346 DGKIGHVWNTMF-----ACDGLGNG-GHFEYVVDKTPYIGDDTSIGRKN 389
 Db 268 -DKMFHFWNTFFIPGPEETSEKVENGLCQOEIDSICTERADNDKEYL----- 316

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QY 390 GMRNETPMRKIDPETGNEFESP 412
Db 317 VLTLTKNDLDRANKDANKRYFSP 339

RESULT 10
US-10-299-003-2
; Sequence 2, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-299-003-2

Query Match 9.5%; Score 490.5; DB 12; Length 403;
Best Local Similarity 31.3%; Pred. No. 9.6e-31;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRATVSSNRCRTEYQNIIDLCAYITDRIIAIGYPATGIEANFRNSKVTOQOFLTRRHGK 107
Db 4 LIKEIVSRNKRRYQEDGFDLDLTIIYPNIIANGPFAERLEGVYRNNDVVRFLDSKH-K 62

QY 108 GNVKFNLRGGYYADNPDGNVICFDMTDHHPSPLELMAPFCRAKEWLEADDKHVIATV 167
Db 63 NHYKIYNLCARHYDTAKFNCRAQYPPEDHNPQLELIKPFCELDQWLSDDDNHVAI 122

QY 168 HCKAGKRGTVMICALLIYINFPSPROILDYYSIIRTKNKGVTIPSORRYIYYHKL 227
Db 123 HCKAGKRGTVMICAYLLHRGKFLKAQALDFYGEVTRDKKGVTPISORRYIYYSYLL 182

QY 228 ERELNYLPLRMQLIGVYVERPPTKWTGGGSKI KVEVNGSTILFKPDPDLIIKSNHQRERA 287
Db 183 KNLHLYRVPALLFKHMFETIPMFSGG-----TCNPQFVVQQLKVKIYSSNSGPTRR- 234

QY 288 TWLNCDTPEFTDGEQKYHGVSKRAYCFMVPEADAPVFEVDVIRIDI--REIGFLKKFS 345
Db 235 -----EDKF-----MYFEFPQPLPVC--GDIKVEFFHKQNKMLKK-- 267

QY 346 DGKIGHVWFTMF-----ACDGLNG-GHFEYVDKTPYIGDDTSIGRKN 389
Db 268 -DKMFHFWNTFFIPGPETSEKVENGLSCDQEIDSICSIERANDNKEYL----- 316

QY 390 GMRNETPMRKIDPETGNEFESP 412
Db 317 VLTLTKNDLDRANKDANKRYFSP 339

RESULT 11
US-10-299-003-10
; Sequence 10, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
```

```
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-299-003-10

Query Match 9.5%; Score 490.5; DB 12; Length 403;
Best Local Similarity 31.3%; Pred. No. 9.6e-31;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRATVSSNRCRTEYQNIIDLCAYITDRIIAIGYPATGIEANFRNSKVTOQOFLTRRHGK 107
Db 4 LIKEIVSRNKRRYQEDGFDLDLTIIYPNIIANGPFAERLEGVYRNNDVVRFLDSKH-K 62

QY 108 GNVKFNLRGGYYADNPDGNVICFDMTDHHPSPLELMAPFCRAKEWLEADDKHVIATV 167
Db 63 NHYKIYNLCARHYDTAKFNCRAQYPPEDHNPQLELIKPFCELDQWLSDDDNHVAI 122

QY 168 HCKAGKRGTVMICALLIYINFPSPROILDYYSIIRTKNKGVTIPSORRYIYYHKL 227
Db 123 HCKAGKRGTVMICAYLLHRGKFLKAQALDFYGEVTRDKKGVTPISORRYIYYSYLL 182

QY 228 ERELNYLPLRMQLIGVYVERPPTKWTGGGSKI KVEVNGSTILFKPDPDLIIKSNHQRERA 287
Db 183 KNLHLYRVPALLFKHMFETIPMFSGG-----TCNPQFVVQQLKVKIYSSNSGPTRR- 234

QY 288 TWLNCDTPEFTDGEQKYHGVSKRAYCFMVPEADAPVFEVDVIRIDI--REIGFLKKFS 345
Db 235 -----EDKF-----MYFEFPQPLPVC--GDIKVEFFHKQNKMLKK-- 267

QY 346 DGKIGHVWFTMF-----ACDGLNG-GHFEYVDKTPYIGDDTSIGRKN 389
Db 268 -DKMFHFWNTFFIPGPETSEKVENGLSCDQEIDSICSIERANDNKEYL----- 316

QY 390 GMRNETPMRKIDPETGNEFESP 412
Db 317 VLTLTKNDLDRANKDANKRYFSP 339

RESULT 12
US-10-299-003-49
; Sequence 49, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
```

```
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 49
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-299-003-49

Query Match
Best Local Similarity 31.3%; Score 490.5; DB 12; Length 403;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRTAVSSNRCTEYQNIIDLCAYITDRIIAIGYPATGIEANFRNSKVQTOQFLTRRHGK 107
Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H - K 62
QY 108 GNVKFNLRGGYYDADNFDGNVICFDMTDHHPSPSLEMAPFCREAKEWLEADDKHVIATV 167
Db 63 NHYKIYNLCABERHYDTAKNCRVAQYFPEDHNPPOLELIKPFCELDQWLSDDNHNVAI 122
QY 168 HCKAGKGRGTGMICALLIYINFPSPROILDYYSIIRTKNNKGVITIPSORRYVYYHKL 227
Db 123 HCKAGKGRGTGMICAYLLHKGFLKAQEAALDFYGEVTRDKKGVITIPSORRYVYYSYLL 182
QY 228 ERELNYPLRMOLIGVYVERPPTKMGWGGSKIKVEVNGSTILFKPDPPLIISKSNHORERA 287
Db 183 KNHLDYRPVALLFHKMFEETIPMSGG-----TCNQFVVCQLKVKIYSSNSGPTTR- 234
QY 288 TWLNNDCTPNEFDTEGQYHGFVSKRAYCFMVPEDAPVFEVDVRI--REIGFLKKFS 345
Db 235 -----EDKF-----MYFEFPQPLPVC--GDIKVEFFHKQKMLKK-- 267
QY 346 DGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIGDTSIGRKN 389
Db 268 -DKMFHFWNTFFPGPEETSEKVENGLSCDEIDSICSIERADNDKEYL----- 316
QY 390 GMRNETPMRKIDPBTGNEPESP 412
Db 317 VLTLTKNDLKDANKDKANRYFSP 339

RESULT 13
US-10-299-003-55
; Sequence 55, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtighian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 55
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-299-003-57

Query Match
Best Local Similarity 31.3%; Score 490.5; DB 12; Length 403;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRTAVSSNRCTEYQNIIDLCAYITDRIIAIGYPATGIEANFRNSKVQTOQFLTRRHGK 107
Db 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H - K 62
QY 108 GNVKFNLRGGYYDADNFDGNVICFDMTDHHPSPSLEMAPFCREAKEWLEADDKHVIATV 167
Db 63 NHYKIYNLCABERHYDTAKNCRVAQYFPEDHNPPOLELIKPFCELDQWLSDDNHNVAI 122
QY 168 HCKAGKGRGTGMICALLIYINFPSPROILDYYSIIRTKNNKGVITIPSORRYVYYHKL 227
Db 123 HCKAGKGRGTGMICAYLLHKGFLKAQEAALDFYGEVTRDKKGVITIPSORRYVYYSYLL 182
QY 228 ERELNYPLRMOLIGVYVERPPTKMGWGGSKIKVEVNGSTILFKPDPPLIISKSNHORERA 287
Db 183 KNHLDYRPVALLFHKMFEETIPMSGG-----TCNQFVVCQLKVKIYSSNSGPTTR- 234
QY 288 TWLNNDCTPNEFDTEGQYHGFVSKRAYCFMVPEDAPVFEVDVRI--REIGFLKKFS 345
Db 235 -----EDKF-----MYFEFPQPLPVC--GDIKVEFFHKQKMLKK-- 267
QY 346 DGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIGDTSIGRKN 389
Db 268 -DKMFHFWNTFFPGPEETSEKVENGLSCDEIDSICSIERADNDKEYL----- 316
QY 390 GMRNETPMRKIDPBTGNEPESP 412
Db 317 VLTLTKNDLKDANKDKANRYFSP 339

RESULT 14
US-10-299-003-57
; Sequence 57, Application US/10299003
; Publication No. US20030139324A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar
; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavtighian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 57
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-299-003-57

Query Match
Best Local Similarity 31.3%; Score 490.5; DB 12; Length 403;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IFRTAVSSNRCTEYQNIIDLCAYITDRIIAIGYPATGIEANFRNSKVQTOQFLTRRHGK 107
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```

Db      4  I I K E I V S R N K R R V Q E D G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H - K 62
QY      108 G N V K V N L R G G Y Y Y D A D N F D G N V I C F D M T D H H P P S L E L M A P F C R E A K E W L E A D D K H V I A V 167
Db      63  N H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A I 122
QY      168 H C K A G K G R T G V M I C A L L I Y I N F P S P R Q I L D Y Y S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 227
Db      123 H C K A G K G R T G V M I C A L L I Y I N F P S P R Q I L D Y Y S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 182
QY      228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E V G N G S T I L F K P D P L I I S K S N H Q R E R A 287
Db      183 K N H L D Y R P V A L L F H K M F E T I P M F S G G - - - - - T C N P Q F V V C Q L K V K I Y S N S G P T R R - 234
QY      288 T W L N N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I - - R E I G F L K K F S 345
Db      235 - - - - - E D K F - - - - - M Y F E F P Q L P V C - - G D I K V E F F H K N K M L K K - - 267
QY      346 D G K I G H V W F N T M F - - - - - A C D G G L N G - G H F E Y V D K T O P Y I G D T S I G R K N 389
Db      268 - D K M F H F W N T F F I P G P E T S E K V E N G S L C D Q E I D S I E R A D N D K E Y L - - - - - 316
QY      390 G M R N E T P M R K I D P E T G N E F E S P 412
Db      317 V L T L T K N D L D K A N K D K A N R Y F S P 339

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RESULT 15
US-10-059-585-50
; Sequence 50, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayaashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-50

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Query Match 9.5%; Score 490.5; DB 15; Length 403;

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Best Local Similarity 31.3%; Pred. No. 9.6e-31;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;
QY      48  I P R T A V S N R O R T E Y Q N I D L D C A Y I T D R I I A I G Y P A T G I E A N F R N S K V Q T O Q F L T R R H G K 107
Db      4  I I K E I V S R N K R R V Q E D G F D L D L T Y I P N I I A M G F P A E R L E G V Y R N I D D V R F L D S K H - K 62
QY      108 G N V K V N L R G G Y Y Y D A D N F D G N V I C F D M T D H H P P S L E L M A P F C R E A K E W L E A D D K H V I A V 167
Db      63  N H Y K I Y N L C A E R H Y D T A K F N C R V A Q Y P F E D H N P P Q L E L I K P F C E D L D Q W L S E D D N H V A I 122
QY      168 H C K A G K G R T G V M I C A L L I Y I N F P S P R Q I L D Y Y S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 227
Db      123 H C K A G K G R T G V M I C A L L I Y I N F P S P R Q I L D Y Y S I I R T K N N K G V T I P S O R R Y I Y Y H K L R 182
QY      228 E R E L N Y L P L R M Q L I G V Y V E R P P K T W G G S K I K V E V G N G S T I L F K P D P L I I S K S N H Q R E R A 287
Db      183 K N H L D Y R P V A L L F H K M F E T I P M F S G G - - - - - T C N P Q F V V C Q L K V K I Y S N S G P T R R - 234
QY      288 T W L N N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I - - R E I G F L K K F S 345
Db      235 - - - - - E D K F - - - - - M Y F E F P Q L P V C - - G D I K V E F F H K N K M L K K - - 267
QY      346 D G K I G H V W F N T M F - - - - - A C D G G L N G - G H F E Y V D K T O P Y I G D T S I G R K N 389
Db      268 - D K M F H F W N T F F I P G P E T S E K V E N G S L C D Q E I D S I E R A D N D K E Y L - - - - - 316
QY      390 G M R N E T P M R K I D P E T G N E F E S P 412
Db      317 V L T L T K N D L D K A N K D K A N R Y F S P 339

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Search completed: December 10, 2003, 20:43:26
Job time : 43.8968 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:30:07 ; Search time 27.8035 Seconds
(without alignments)
3327.436 Million cell updates/sec

Title: US-09-205-658A-310
Perfect score: 5168
Sequence: 1 MVTPEPDPVSTSTRSMARDL.....IAHPSEFSDSNFDQAIYL 962

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

				SUMMARIES					
Result No.	Score	Query Match %	Length	ID	Description				
1	5168	100.0	962	T51924	daf-18 protein - C				
2	5156.5	99.8	965	T32574	hypothetical prote				
3	437	8.5	628	T45864	probable tyrosine				
4	283	5.5	1792	T45075	tensin - chicken (
5	281	5.4	1744	T45070	tensin - chicken				
6	271.5	5.3	1733	T27939	protein-tyrosine p				
7	247.5	4.8	348	T40573	auxilin - bovine				
8	217.5	4.2	910	T68983	cyclin G-associate				
9	217.5	4.2	1305	T31096	probable tyrosine				
10	209.5	4.1	434	T53155	glutamate rich pro				
11	162	3.1	1271	T45555	hypothetical prote				
12	154	3.0	446	T33986	protein FicA4.2 [
13	149	2.9	736	T86271	repeat organellar				
14	146.5	2.8	1939	T18372	probable protein-t				
15	141	2.7	537	T50099	hypothetical prote				
16	140	2.7	981	T05505	giantin - human				
17	138.5	2.7	3259	A56539	giantin - human				
18	137.5	2.7	3225	T52300	hypothetical prote				
19	136	2.6	993	T90072	hypothetical prote				
20	136	2.6	1053	T34172	sucrose-phosphate				
21	135	2.6	834	T57282	ankyrin-related pr				
22	135	2.6	1166	T28680	fibrinogen-binding				
23	134.5	2.6	6642	T29757	protein UNC-89 - C				
24	133	2.6	264	T25762	hypothetical prote				
25	133	2.6	5170	T15348	hypothetical prote				
26	132.5	2.6	1244	T19068	hypothetical prote				
27	131	2.5	3824	T37431	ankyrin 2, neuroa				
28	130.5	2.5	1054	T09833	sucrose-phosphate				
29	130.5	2.5	1863	A58881	breast/ovarian can				

30 130.5 2.5 1955 2 T30934 myosin-like protei
31 129.5 2.5 786 2 A59339 kinesin homolog KH
32 129.5 2.5 1226 2 S15053 hypothetical prote
33 129 2.5 1871 2 D96796 probable heat shoc
34 128.5 2.5 1195 1 S26722 DNA-directed RNA p
35 128 2.5 1141 2 S89824 hypothetical prote
36 128 2.5 3147 2 T18674 hypothetical prote
37 127.5 2.5 1142 2 S59359 GIN4 protein - yea
38 127.5 2.5 5327 2 T13564 microtubule-associ
39 127 2.5 1507 2 B47328 natural killer cel
40 126.5 2.4 1616 2 G64242 cytodherence-acces
41 126.5 2.4 2039 2 T15347 ankyrin-related un
42 125.5 2.4 2104 2 T38774 myosin-3 heavy cha
43 125 2.4 2722 2 T20532 hypothetical prote
44 125 2.4 427 2 S38002 hypothetical prote
45 125 2.4 790 2 T05576 hypothetical prote

ALIGNMENTS

RESULT 1

T51924
daf-18 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C:Accession: T51924
R:OGG, S.; Ruvkun, G.
Mol. Cell 2, 887-893, 1998
A:Title: The C. elegans PTEN homolog DAF-18 acts in the insulin receptor-like metabolic
A:Reference number: Z25864
A:Accession: T51924
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-962 <OGG>
A:Cross-references: EMBL:AF098286; PIDN:AAD03420.1
C:Genetics:
A:Gene: daf-18

Query Match 100.0%; Score 5168; DB 2; Length 962;
Best Local Similarity 100.0%; Pred. No. 1.1e-317;
Matches 962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTPEPDPVSTSTRSMARDLQENPNRQCEPRVSEPYHNSIVIRIRHIFRTAVSSNRCRT 60
DB 1 MVTPEPDPVSTSTRSMARDLQENPNRQCEPRVSEPYHNSIVIRIRHIFRTAVSSNRCRT 60
QY 61 EYQNIIDLCAYITDRIIAIGYPATGIEANFNRSKVQTOQFLTRRHGKGNVFNLRGGY 120
DB 61 EYQNIIDLCAYITDRIIAIGYPATGIEANFNRSKVQTOQFLTRRHGKGNVFNLRGGY 120
QY 121 YDADNFDGNCVCFDMTDHPPSLELMAPFCREAKEWLEADDKHVIAVHCKAGKGRGTGVI 180
DB 121 YDADNFDGNCVCFDMTDHPPSLELMAPFCREAKEWLEADDKHVIAVHCKAGKGRGTGVI 180
QY 181 CALLIYINFPSPROILDYISIRTKNNKNGVTIPSQRRYIYYHKLRELNLYPLRMQL 240
DB 181 CALLIYINFPSPROILDYISIRTKNNKNGVTIPSQRRYIYYHKLRELNLYPLRMQL 240
QY 241 IGVYVERPKTWGGSGSKIKVEVGNGSTILFKPDPLIISKSNHQRERATWLNCCDTPNEPD 300
DB 241 IGVYVERPKTWGGSGSKIKVEVGNGSTILFKPDPLIISKSNHQRERATWLNCCDTPNEPD 300
QY 301 TGEQKYHGFVSKRAYCFWVPEDAPVFEVDGVRIDIREIGFLKKPSDGKIGHVWNTMFAC 360
DB 301 TGEQKYHGFVSKRAYCFWVPEDAPVFEVDGVRIDIREIGFLKKPSDGKIGHVWNTMFAC 360
QY 361 DGLNGGHFEYVDKTPQYIGDDTISGRKNGMRNETPMRKIDPDTGNFEFESQWVNPFG 420
DB 361 DGLNGGHFEYVDKTPQYIGDDTISGRKNGMRNETPMRKIDPDTGNFEFESQWVNPFG 420
QY 421 LEKHITESQAMENYNYGMIPRYTISKILHEKHEKGVKDDYNDNRKUPMGDKSVTESGK 480
DB 421 LEKHITESQAMENYNYGMIPRYTISKILHEKHEKGVKDDYNDNRKUPMGDKSVTESGK 480

A:Residues: 1-628 <BAR>
A:Cross-references: EMBL:AL132978
A:Experimental source: cultivar Columbia; BAC clone F3A4
C:Genetics:
A:Map position: 3
A:Introns: 192/3; 226/3; 245/3; 267/3; 326/3; 355/3; 377/2; 399/1; 414/3; 458/2; 481/3
A:Note: F3A4.190

Query Match 8.5%; Score 437; DB 2; Length 628;
Best Local Similarity 25.5%; Pred. No. 1e-19;
Matches 156; Conservative 80; Mismatches 195; Indels 180; Gaps 26;

QY 3 TTPDPVPSSTSMARDL--QENNR-----RIRHIFRTAVSSNCRTEYQINIDLCAYITDR 75
Db 91 SPSPISFSSGLSWAKSFKFQDDPNRTDGSMAFRTSELGLHLPTKSGSEVGDGRS 150
QY 35 -----EPYNSIVE-----RIRHIFRTAVSSNCRTEYQINIDLCAYITDR 75
Db 151 NTQVGAFESLTKAVVDSRGAVKAMQVKARH-----VSQNKRYQEGEFDLDMYITEN 206
QY 76 IIAIGYPATGI-----EAFNRSKVQTQOFLTRRHGKGNVKNVFNLRGGYYADNPD 127
Db 207 IIAAGPPAGDISGLFGFEGLYRNHMEVIRKFFETH--KDKYKVNLCSERLYDASRE 265
QY 128 GNVICFDMTDHPPPSLEMAPCEKAEKLEADDKHVIACHKAGKAGRTGVMICALLIYI 187
Db 266 GKVASFPFDDHNCPPQLIPSCQSAITWLKEDIQNVVVVCHKAGMARTGLMICCLLYL 325
QY 188 NFYPPKQILDYYSIIRTKNNKGVITPSORRYIYYHKLRLERLNVLPUR---MOLIGV- 243
Db 326 KFEPTAEAAIDYNNQKCLDGKALVLPQIRVYKYYERVQNFQDGKVPERRGRLINCP 385
QY 244 YVERPPKTVGGGSKIKVEVNGSTILFKPDPLIISKSNHQRERATWLNCDTPEFDTGE 303
Db 386 WYIRP-----AITISNTHDLF-----STKHQKTK-----DLGP 415
QY 304 QKYHGFVSKR--AYCFMVPEDAPVF--VEGDVDRIDIREIGFLKFKSDGKIGHVFNWTFMFA-- 359
Db 416 EDFWIKAPKGGVVVFAIPGEAGLTLAGDFKIHFD-----SDGDF--YCLWLTTLTDN 467
QY 360 -----CDG-----GLNGHFYV---DKTQP-----YIGDDTSIGRKNR 392
Db 468 RTWLKSGDFDGRKRLPAGFHEIVMTEPNSSQTKSKSDSTQOQSSSSAASSKUK 527
QY 393 RNETPMRKIDPTEGNEFESPMQIVNPPGLEKHITTEQAMENYTYGMIPRYTISKILHE 452
Db 528 SNEKDDVPSDSGEE-----EGNSQSYSTNEKTASSMHTTSK--PHQ 568
QY 453 KHEKGLVKDDYNDKRLPMGDKSYTESGKSG-----DIRVGGPPEIPYKAE 499
Db 569 INEPP--KRDD-----PSANRSVTSSSSSGHYNPINNSLAVSDIKAIA-----ADA 613
QY 500 HVLTPVYEMD 510
Db 614 SVFSGDEED 624

RESULT 4
A57075
tensin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 21-Jul-2000
C:Accession: A57075
J:Chuang, J.Z.; Lin, D.C.; Lin, S.
R:Cell Biol. 128, 1095-1109, 1995.
A:Title: Molecular cloning, expression, and mapping of the high affinity actin-capping c
A:Reference number: A57075; MUID:95204530; PMID:7896874
A:Accession: A57075
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-11792 <CHU>
A:Cross-references: GB:I06662; NID:G212754; PIDN:AAA73949.1; PID:G212755
C:Superfamily: SH2 homology

F.1520-1629/Domain: SH2 homology <SH2>

Query Match 5.5%; Score 283; DB 2; Length 1792;
Best Local Similarity 20.5%; Pred. No. 2.5e-09;
Matches 172; Conservative 94; Mismatches 252; Indels 322; Gaps 32;

QY 2 VTTPDPVSTSTRWARDLQENPNRQCPGEPRVSEPHNSIVERIHRIFRTAVSSNCRTE 61
Db 77 ITKQVDTDP--ATRS-----PRGQAHKA-----SRSMSTVATATESC--- 113
QY 62 YQNIIDLCAYITDRIIAGYPATGTEANFRNSKVOTQOFLTRRHGKGNVKNVFNLRGGYY 121
Db 114 -----ELDLVYITERIIAVSYFSTAEQFSRNLREVAHMLKSKG--DNYVLNL--SERH 167
QY 122 DADNPDGNGVICFDMTDHPPPSLEMAPCEKAEKLEADDKHVIACHKAGKAGRTGVMIC 181
Db 168 DISKLHPKVLDGFWPDLHTPALEKICSICKAMDWLNAAAHNVVVLHNGRGLGVVA 227
QY 182 ALLIYINFPSPQILDYYSIIRTKNNKGVIT--PSQRYIYYHKLRLER--ELNVLPUR 237
Db 228 AYMHYSNTSASADQALDRFAMKRFYEDKVVPVQPSQKRYIHYFSGLLSGSIKMNKPLF 287
QY 238 MQ-----LIGVYVERPPKTVGGGSKIKVEVNGSTILFKPDPL--- 275
Db 288 LHHVIMHGIPIPFESGCGRPFLKIYQAMQPVVTSGIYVNGSQTGICITIEPGLLKG 347
QY 276 IISKSNHQRERATWLNCDTPEFDTGEQKYGKVFVSKRAYCFMVPEDAPVFVEGDVRI 335
Db 348 ILLKCYHKKF-----SPTRDVIFRQFH-----TCAVHDLDI--VFGEKDLDEAF 391
QY 336 REIGFLKFKSD--GKIGHVFNWTFMPCDGLNGHGFYVDKTOPYIGDDTSIGRKNR 394
Db 392 RD-----ERFPEYKGVFV-----FSY----- 408
QY 395 ETPMERKIDPTEGNEFESPMQIVNPPGLEKHITTEQAMENYTYGMIPRYTISKILHE 454
Db 409 -----GPEK-----IQMEHLENGPSVSDVINTSDPL--- 435
QY 455 EKGIVKDDYNDKRLPMGDKSYTESGKSGDIRGVGPFPIPYKAEHVLTPFVYEMDRALK 514
Db 436 ---IRWDSYENFNIREDS-----EGTWAEPALPGKHEKVEGHTQGLDGLSY 482
QY 515 SKDLNNGKLVHLVCVTRDSKMEKSEVFNGLAFHNESTRRLQALTOGNPKWRPEPCA 574
Db 483 -----AKVKKDSLHSGISGAVNAARPLSA----- 507
QY 575 FGSKGAEMHYPPSVYSSNDGKYNCASENLSVDFEHRNIAVLNRYCRYFYKQSTSR 634
Db 508 -----APNHVEHTLSVSDSG-----NSTAST 529
QY 635 RYPRKFRYCPLIKKHFIYPADTDDVDENGQPPFH---SPEHYIKQEOKIDAEKAAKG 691
Db 530 KTDR-----TDEPGAPGPTGHAVLSPE-----EKRELDRLILVFGLES 568
QY 692 TGPSTSGSAPGTIKKTEASQSDKVKPATEDELPPARLPDNNRVRPFVGVDFENPEESC 751
Db 569 APP--MNHAPG-----PA-----PARLP----- 585
QY 752 EHKTVESITAGPEPLEHFLFESHVHPNTAGNMLRDQVHTDSEVKIAEQEAKAFVDOLLNG 811
Db 586 -----AG--PGRHVVPVPAQVHVNGAGTPL-----LAERETDILDDELPNODG 624

RESULT 5
A54970
tensin, cardiac muscle - chicken
C:Species: Gallus gallus (chicken)
C>Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 21-Jul-2000
C:Accession: A54970; S38330; S21544
R:Lo, S.H.; An, Q.; Bao, S.; Wong, W.K.; Liu, Y.; Janney, P.A.; Hartwig, J.H.; Chen, L.B
J:Bio. Chem. 269, 22310-22319, 1994
A:Title: Molecular cloning of chick cardiac muscle tensin. Full-length cDNA sequence, e
A:Reference number: A54970; MUID:94350987; PMID:8071358

QY 574 AFGSKGAEMHYPPSVRYSSNDKYNACSENLSVDFEHRNIAVLNRYCRYFYKORSTSR 633
Db 461 -----APNVEHTLSVSDSG-----NSTAS 481
QY 634 SRYPRKFRYCLPKKHGFIPADTDVDVNGQPFHSPHYIKQSKDAEK--AAKGLEN 691
Db 482 TK-----TDRTEFGAPGATGHAVALSPKRDVDRLLVFGFLES 521
QY 692 TQPTSGSSAPOTIKKTBASQDKVKPATEDBLPARLPDNRVRFPVGVDFENPEBSC 751
Db 522 AAP--MHNHAPG-----PA-----DARLP----- 538
QY 752 EHKTVESITAGPEPLHSPHESVHPNTAGNMLRQDVTSEVKIAFOEAKAFVDQLLNGQ 811
Db 539 -----AG--PGRHVVPQVHVNGAGTPL-----LABRETDLDDLPNQDG 577

RESULT 7

T40573

protein-tyrosine phosphatase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40573

R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrall, B.G.

submitted to the EMBL Data Library, January 1999

A:Reference number: Z1938

A:Accession: T40573

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-348 <SEE>

A:Cross-references: EMBL:AL035226; PIDN:CAA22831.1; GSPDB:GN00067

A:Experimental source: strain 972h; cosmid c609

C:Genetics:

A:Gene: SPAC609.02

A:Map position: 2

Query Match 4.8%; Score 247.5; DB 2; Length 348;
Best Local Similarity 33.5%; Pred. No. 3.8e-08;
Matches 65; Conservative 33; Mismatches 87; Indels 9; Gaps 5;

QY 47 HIFRTAVSSNRCTRYQVID-----LDCAIITDRIIAIGYPATGTEANFRNSKVQTOQL 101
Db 2 NILRSVSRGKGLQKQKNRSFAVLDVYITTSKVIAMSTPAAGTHKJRNDELDFVKYL 61
QY 102 TRRHGKGNVKFNL-RGGYYVDADNFDGNVICFDMTDHHPPLSLELMAPFCREAKEWLEAD 160
Db 62 TTQL-KDNWILLNLCAEETVYHLEFKPNVINYQDNPPPLFLWALVNMMDALFQTL 120
QY 161 DKHVIATVHCAGKGTGWMICALLIYINFPSPROIIDYYSIIRTKNNKGVTPSQRYI 220
Db 121 PLLTIVVHCAGKGTGTGVCISYLVAFGL-TAKQSELYTEKRMVRGHGLTISQIRYV 179
QY * 221 VYHKLRERELNYL 234
Db 180 YIIEILKQFP-NYL 192

RESULT 8

S68983

auxilin - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 08-Oct-1999

C:Accession: S68983

R:Schroeder, S.; Morris, S.A.; Knorr, R.; Plessmann, U.; Weber, K.; Vinh, N.G.; Ungewick

Eur. J. Biochem. 228, 297-304, 1995

A:Title: Primary structure of the neuronal clathrin-associated protein auxilin and its e

A:Reference number: S68983; MUID:95220355; PMID:7705342

A:Accession: S68983

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-910 <SCH>

A:Cross-references: EMBL:U09237; NID:G485268; PIDN:AAA79037.1; PID:G485269

C:Superfamily: dnaJ amino-terminal homology

F:846-910/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 4.2%; Score 217.5; DB 2; Length 910;
Best Local Similarity 21.0%; Pred. No. 1.2e-05;
Matches 211; Conservative 115; Mismatches 371; Indels 307; Gaps 52;

QY 60 TEYNIDLDCAIITDRIIAIGYPATGTEANFRNSKVQTOQLTRRHGKGNVKVFNLRGY 119
Db 54 TSYTKGDLDFYVTSRIIVMSFPLDSVDIGFRNQVDIIRSFDSRH-LDHVTYVNLSPKS 112
QY 120 YYDADNFDGNVICFDMTDHHPPLSLELMAPFCREAKEWLEADDKVIAVHCAGKGRTCVM 179
Db 113 YRTA-KHRSRVSECSWPRIQAPSLHNLPAVCNRMVNWLLQNPKNVCVCHLDGRAASIL 171
QY 180 ICALLIYINFY--PSPROIIDYYSIIRTKNNKGVTI-PSORRYIYYHYKL----RERELNY 233
Db 172 VGAMFICNLYSTFGPAVRLLY-----AKRPGIGLSFSHRRYLGCMCDLLADKPYRPHF 225
QY 234 LPLRMQLIGVYVVRPPKWTGGGSKIKEVGVNGSTILFKPDDLIIISKSHQERATWLNMC 293
Db 226 KPLTIKSIIV-----SPVPFF-----NKQR-----NGC 248
QY 294 DTPNEFDTGEOKYH---GFVSKRAYCFMWPEADPVF-----VEGDVRIIDIRET---- 338
Db 249 RPYCDVLIGETKIYTTCADFERMKEYRV---QDKIFIPLSITVQGDVVVSMYHLRSTIG 305
QY 339 -GFLKFSFDGKIGHWFTNMF-----ACDGLNGGHFYYVDKTPQYIGD 381
Db 306 SRLQAKVNTQIFQLQFHTGFIPLDTTVLTKFTKPELDACD-----VPEKYPQLFQ 355
QY 382 DTSIGRKNRMNETPMRKIDPETGNFESPWQ-----IVNPPGLEKHIITEQAMENVTN 436
Db 356 VT-----LDVELQPHDKV-----MELTPPWEHYCTKDVNPSILFSSHQHQ--DTLVL 401
QY 437 YGMIP-----PRY-----TISKIL--HEKHEGIVKDDY---NDRKLPWGDKSYTES 478
Db 402 GGOAPIDIPNPNRHFQGGFFSTLCWQDQKSEKFCFEEHAALVNQSESDDELLTIS 461
QY 479 KSGSDIRGVGFFPIPY-----KABEHVLITFPVYEMD-----RALKSKDLNNGMKLHV 526
Db 462 SPHNGANG-----DKPHAARKPSKQEPAPAPEDVDVLLGLESAVSKNFSS----- 510
QY 527 VLRCVDTSDSKOMKSEVFG-----NLAHF-----NEST-RRIQALQTM 564
Db 511 --PAAPPSNSELL--SOLFSGGGAAGPVQSGQGVDDVFHPSPGPTSTOSTPRRSATSTA 566
QY 565 NPKTR-PEPCAFGSKGAEMHYPPSVRYSSND--GKYNACSENLSVDFEHRNIAVLNRY 621
Db 567 SPTLRVGEATFDFFGA-----PS-KPSGQDLGSLNTASAS--SDPF----- 607
QY 622 CRYFYKORSTSRSPRKYRCPLIKKHFIYPADTDVDVNGQPFHSPH-PEHYIKEOEKI 680
Db 608 ---LQPTFSPTVHASS-----TPAVNIQPDVSGANDWHTKPGFP----- 645
QY 681 DAEKAAKGIENGTGSTGSS-----APQTIKK-----TEASQSKVKPATEDEL--- 724
Db 646 ----GMGSKSAATSPGSSHGTPHQNKPTLPDFADLGTGGSSFAKSPSTPTGLGGG 700
QY 725 -PPARLPDNRVRFPVVG-----VDPENPEESCEHKTVESIAGFLEHLPHESY 773
Db 701 FFLSSPQKASFPQMGWGQGGYNNWQQTQKPSMHPHSSPQNRPN-----YVNSF 753
QY 774 HPNTAGNMLRQDHYTDSVKIAEOAKAFVDQLLNGQGVLFQEFMKQKQFVPSDNSFADYVT 833
Db 754 SSMFGGQNERKAAANLEGG--OKAADFED-LLSGQG-----FNAHKDK----- 794
QY 834 GOAEVFAQIALLQSEDFORVQNAEVEVDLEHTLGEAFERFGHVHVESNGSSKNPKALK 893
Db 795 -----KGPRTIAB-----MRKEEMAKEMDPEKL-----KILEWIEGKERNIRALL 834
QY 894 TREOMVETGDKTOKTRNHLVLLHLEAHRVQIERRETCPHELHPE 937
Db 835 STMHTVLWAGETKWKVPG--MADLVTPQEVKKVYKAVLVVHPD 876

RESULT 9

T31096
 cyclin G-associated kinase GAK - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T31096
 R:Kanaka, Y.; Kimura, S.H.; Okazaki, I.; Ikeda, M.; Nojima, H.
 FBS Lett. 402, 73-80, 1997
 A:Title: GAK: a cyclin G-associated kinase contains a tensin/auxilin-like domain.
 A:Reference number: Z20979; MUID:97165969; PMID:9013862
 A:Accession: T31096
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1305 <KAN>
 A:Cross-references: EMBL:D38560; NID:g1902912; PIDN:BAAL8911.1; PID:g1902913
 A:Note: GAK and cyclin G associate together in vivo
 C:Genetics:
 A:Gene: GAK

Query Match	4.2%	Score 217.5;	DB 2;	Length 1305;
Best Local Similarity	22.1%;	Pred. No. 2.1e-05;		
Matches	92;	Conservative 56;	Mismatches 161;	Indels 107; Gaps 17;

QY 62 YQNIDLCAYITDRIIAIGYPATGTEANFRNSKVQTOQLTRRHGKGNVKNLGGVYY 121
 DB 401 YAKGDLDTSYITSRIAVMSFPAEGVESAIKNKNIEDVRLFLDAKH-PGHVAVYNL-SPRIY 458

QY 122 DADNFDGNVICFDMTDHPPSLMAPPFCREAKEWLEADDKHVIADVHCKAGKGRGVMIC 181
 DB 459 RASKFNRVTECGWAVRRAPHLHSLYTLCSRHAWLREDRNVCVVCHMDGRAASAVVC 518

QY 182 ALLIYINFPSPRQILDYYSIIRTKNNKGVTPISQRRYIYYHKLRELYNLPLRMQI 241
 DB 519 AFLCFRLPSTAAAVYMFMSKRCP--PGIW-PSHKRYIEY-----VC 558

QY 242 GYVVERPPKTTGGGSKIKVEGVNGSTILFKPDPPLIISKNHOR-----ERATLNN 292
 DB 559 DMVAEPIPTHSKPLVK-----SVNTPVPLFSKQNRGCRPFCEVYVGEERV----- 607

QY 293 CDTNFEFDGEOYHGFVSKRAYCFMVPEADPVF-----VEGDVIRIDREI-----GFLK 342
 DB 608 -TTSQBYDMKE-----FKIEDGKAVIPGIVQGDVLTIIHARSTIGRLQ 654

QY 343 -RPSDGKIGHVFNFTMF-----ACDGLNGGHFEYVDKTPQYIGDDTSI 385
 DB 655 AKWASKMFQIQPHTGFVPRNATTVKFAKYDLDAKD-----IQEKYP---DLFQV 701

QY 386 GRKNGHRRNETPWRKIDPETGNEFSPWQIVNPPGLEKH-----TERQAMENTNYG 438
 DB 702 NLEVEVEPRDRPSRDV-----PPWENTSRLRGLNPKILFSNRREEQQDILSKFG 748

RESULT 10

S55155
 probable tyrosine phosphatase YNL128w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: probable tyrosine phosphatase N1220; protein JTB434; protein N1972
 C:Species: Saccharomyces cerevisiae
 C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
 C:Accession: S55155; S59260; S63073
 R:Mallet, L.; Bussereau, F.; Jacquet, M.
 submitted to the EMBL Data Library, November 1994
 A:Description: A 43.5 kb fragment of the chromosome XIV.
 A:Reference number: S55136
 A:Accession: S55155
 A:Molecule type: DNA
 A:Residues: 1-434 <NAL>
 A:Cross-references: EMBL:Z46843; NID:g861113; PID:g854509
 R:Mallet, L.; Bussereau, F.; Jacquet, M.
 Yeast 11, 1195-1209, 1995
 A:Title: A 43.5 kb segment of yeast chromosome XIV, which contains MFA2, MEP2, CAP/SRV2,
 A:Reference number: S59241; MUID:96109932; PMID:8619318

A:Accession: S59260
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-434 <MAW>
 A:Cross-references: EMBL:Z46843; NID:g861113; PIDN:CAA86897.1; PID:g854509
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994
 R:Mallet, L.; Bussereau, F.; Jacquet, M.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63069
 A:Accession: S63073
 A:Molecule type: DNA
 A:Residues: 1-434 <MAP>
 A:Cross-references: EMBL:Z71404; NID:g1302063; PID:e239804; PID:g1302064; MIPS:YNL128w
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:TEP1
 A:Cross-references: SGD:S0005072; MIPS:YNL128w
 A:Map position: 14L
 C:Keywords: transmembrane protein
 F:38-54/Domain: transmembrane #status predicted <TM1>

Query Match	4.1%	Score 209.5;	DB 2;	Length 434;
Best Local Similarity	23.8%;	Pred. No. 1.3e-05;		
Matches	91;	Conservative 44;	Mismatches 146;	Indels 101; Gaps 15;

QY 67 LDCAIITDRIIAIGYPA-TGTEANFRNSKVQTOQLTRRHGKGNVKNLGGVYY 121
 DB 42 LDISYILVNLVCSYPVNTYPKLLYRNSLDDLLFLTVYHKGNFRIFRGKEDSDYK 101

QY 122 DAD-----NFD-----GNVIC--FDMTD 137
 DB 102 DNDLIGIAAKFESKDFEQLRSLTINDGKIPIPIDLRTLTVEETNNVICERIGWLD 161

QY 138 HHPSPLEMAPFCREAKEWLEADDKHVIADVHCKAGKGRGVMICALLI-YNFYVSPRQI 196
 DB 162 HFPFPFELLEIEVDIGIENYLSVKNRVAVLHCRMGKGRSGMITVAYLMKYLQCPGLEARL 221

QY 197 LDYYSIIRTKNNKGVTPISQRRYIYY-----HKLRELYNLPLRMQILGYVVERPPKT 251
 DB 222 IFMQARFYKGTNGVTIPISQLRYLRYHEFFITHKAAQE-----GISNE----- 265

QY 252 WGGGSKIKEVGVNGSTILFKPDPPLIISKSNHQRERATLNNCDTPNEFDTGQKHYGFVS 311
 DB 266 ---AVKFKFKELAKWTFRLRSSLITSESAIVTTKIQHYN--DORNALLTRKVVYSDIMA 320

QY 312 KRA---YCFMVPEADPVVEGDVIRIDREIIGFLKKFSDGKI-----GHVWFNTMFACDG 362
 DB 321 HECGGMFTFIFGRDY-LTLENDCRIF-TLGTSKSKAASSIISWTSCASCWLN----- 372

QY 363 GLNGHGFYVDKTPQYIGDDTS 384
 DB 373 -----YLETLMHIIKDDSS 386

RESULT 11

A45555
 glutamate rich protein - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jun-2000
 C:Accession: A45555; S27831
 R:Barre, M.B.; Dziegiel, M.; Hough, B.; Petersen, E.; Rieneck, K.; Riley, J.F.;
 J. Mol. Biochem. Parasitol. 49, 119-131, 1991
 A:Title: Primary structure and localization of a conserved immunogenic Plasmodium falciparum life cycle.
 A:Reference number: A45555; MUID:92131041; PMID:1775153
 A:Accession: A45555
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1271 <BOR>
 A:Cross-references: EMBL:M59706; NID:g160311; PID:g160312
 A:Note: sequence extracted from NCBI backbone (NCBIN:77801, NCBIP:77802)

[illegible]

A:Molecule type: DNA
 A:Residues: 1-736 <STO>
 A:Cross-references: GB:AE005172; NID:98778384; PIDN:AAF79392.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F16A14.2
 A:Map position: 1

Query Match 2.9%; Score 149; DB 2; Length 736;
 Best Local Similarity 20.3%; Pred. No. 0.19;
 Matches 150; Conservative 102; Mismatches 260; Indels 228; Gaps 39;

QY 218 RYIVYVHLKLER-----ELNVLPLRMQLIGVYVERPKTWGGGSGIKVEVNGSTILF 270
 DB 77 RYWKYLRPRPRPSPTSDVSLP-KSEFTGKW-KSTLSITTEGEFITE-NSSSPHIV 133

QY 271 KPDPLIISKNSHQREATWLNCDTPNEFDTEGEYKHGVSKRAYCFMVPEDAPVFEVD 330
 DB 134 KAEPKFVSGDGRSGSEERLKFSDKDPDFSFNEDKSY-----PAKRPLCLVSGA 181

QY 331 VRID--IREIGFLKFS-----DGKIGHVWNTMFACDGGGLNGHPEY 371
 DB 182 KEGDEPVQIRIGLSHGASFAPTYVQKLVSLGAGNGDQMYVHPW-----KGILANKRTF 234

QY 372 VDKTPYIGDDTSIGRKGMRNETPMRKIDP-----ETG--NEFESPQIVNPPGL 421
 DB 235 NEKTRKYAGESGSKIPEDLIKGFNP-HKVTPLWNGRLGFTGFAIVDFGKW-----285

QY 422 EXHITBEQAMENYNYGMIPPRYTISKILHEKHE-----KGIV--KDYNDORKLPM 470
 DB 286 -----EGFRNATMFKHFEVSQCGKRDHLTRDPGDKLYGWVAKQDDYYSR-TAI 334

QY 471 GDSYTESGSGDIRGVGPFPIPYKAEHVLTFP-VYEMDRALKSKDLNNGKHLVLR 529
 DB 335 GD-----HLRKQDGLKSVSGK-----BAEDQRKFTLLVSNLENTLVTKSDNLOQMESIYKQ 385

QY 530 CVDTRDSKMKSEVFGNLAFLHNESTRRLQALTMNPKWRPBPAPGSGAEMHYPPSVR 589
 DB 386 TSVLEKRMKEKDEMINT--HNEKMSIMQOTAR-----DYLASI- 422

QY 590 YSNDGKYNGACSENILVDPFFEHRTAVLNRYCRYFYKORSTSRYP-RKFRYCPLIKK 648
 DB 423 YEEHE-----KASQHLEAQKEYED-----RENYDKCAQAKTERRKLQW---QK 465

QY 649 HFVIPADTDDVDENGQPFPHSBEHYKE-----QEKIDAKAAK-----CI 689
 DB 466 HKNLMA-TOQNKADEMMRLABQOQREKDELKQVRELEKIDABQALBELIERMRGDL 524

QY 690 ENTGPSTGSSAPGTIK--KTEASQSK-----VKPA-TEDELPPAR- 728
 DB 525 QVNGHMQEGEGEDSKIKEMIEKTEKEEDWEYQESLYQTLVYVGHGYTDELQDARK 584

QY 729 -LPDNRVRFPV-----VGVDNFENPESCEHK--TVESIAGFPEPL-----EHLFHS 772
 DB 585 ALIRSMRELTTRAYIGVKRMGALDETFFKKVAKEYPAVEADKABELCSLWEEHLGDSA 644

QY 773 YNPNTAGNMLRDYHTDSEVKTAEQAKAFVOLLNGQGVLOPFMFKVPSDNPADYV 832
 DB 645 WHP-----IKVVEKDGLA-KEELNEEDELQELRKL-----675

QY 833 TGOAEVFKAQIALLEQSEDF 852
 DB 676 -GE-EVYAAVTQALKERNEY 693

RESULT 14
 T18372
 repeat organellar protein - Plasmodium chabaudi
 C:Species: Plasmodium chabaudi
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T18372
 R:Werner, E.B.; Taylor, W.R.; Holder, A.A.
 Mol. Biochem. Parasitol. 94, 185-196, 1998
 A:Title: A Plasmodium chabaudi protein contains a repetitive region with a predicted sp

A:Reference number: Z18922; MUID:98418765; PMID:9747969
 A:Accession: T18372
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1939 <MER>
 A:Cross-references: EMBL:U43145; NID:g1151157; PID:g1151158; PIDN:AA63403.1

Query Match 2.8%; Score 146.5; DB 2; Length 1939;
 Best Local Similarity 18.5%; Pred. No. 1.1;
 Matches 180; Conservative 152; Mismatches 368; Indels 273; Gaps 43;

QY 86 IEAFNRNSKVTOQFLTRRHGKGVNFKVFNLRGGYVYDADNFDGNVICPDMTHHPHSL 145
 DB 144 LNLNKENKINKEITL--KREKLNIDIESEYI--EKNKEKELNVEV-NIKMSLDK 197

QY 146 MAPFCREAKLEWLEADKHVIAVHCAGKRGTVGMICALLIYINFPSPQILDDYYSIIRT 205
 DB 198 LTCVQVEKKDLNKKVIEKENNRLK-----EFMKEXNEIIE--SLDGT 243

QY 206 KNNK-----GVTPISQRRYIYY--HKLRERELNYLPLRMQLIGVYVERPPKTWGGGSK 257
 DB 244 INDKNAVEKLEISFEKKRMIEMLDKLEKENF-----279

QY 258 IKVEVNGSTILFKPDPLIISKNSHQREATWLNCDTPNEFDTEGEYKHGF-----309
 DB 280 -----ANKQAKLEKENEIIIEKLDIESR-----EKDFKSEKEKFAEMENELNLT 325

QY 310 --VSKRA-----YCFMVPEDAPVFEVDVRIDIREIGLKKPDSGDKIOWHWNFWTFACDG 362
 DB 326 SDSLKNAQMEVYKLEIKDLSQSLVEKE-----REIFEIKNEYDDKINNMKEKLSINDK 380

QY 363 GLNGHGFYVDTOPYIGDDTSIGRKGMRNETPMRKIDPDTGNEPESQIVN--PPG 420
 DB 381 G-----IDNTVLH--SEEEKINKL--LKEKETELNEIHKYKYLEIETIKNELKEKEE 429

QY 421 LEK-----HITE-----EQAMENYNYGMIPPRYTISKILHEKHEKGIKVD 461
 DB 430 LEKQKKAHTVEVNTLKEIKLEKTEDEKKEGHN-----ELNENLQSLKNEKD 481

QY 462 DYNDRKLPMDGKSYTESGSGDIRGVGPFPIPYKAEHVLTFPVEYEMDRALKS-KDLNN 520
 DB 482 NIKNENTELNDKISS-----LNSEVNLNKKQKTLGNDIKTLNDLIN 523

QY 521 GKMLHVLRCVDTRDSKMKSEVFGNLAFLHNESTR-RLOALTMNPKWRPBPAPGSGSK 579
 DB 524 NLKNE-----INTSNKRNKWK-----DLAMLENEWEGKCVVIDEIKYKKEIFMLESK- 574

QY 580 AEMHYPPSVRYSSNDGKYNGACS--ENLV-----SDFFEHRTAVLNRYCRYFYK 627
 DB 575 -----LKEKENVADLNDEISILRNSIYVKEKEFIEMKEFYENK----INLFPKNFEE 622

QY 628 QR-----STSRSRYPKRYCPLIKKHFIYIPADTDDVDENGQPFPHSBEHYKEQB-- 678
 DB 623 KKNYIENELNSURLKYDNE--QGLIKQ-----IDELNIQKLKTEEKYLQLYNDN 669

QY 679 -----KDAEAKAGIENTGSTSGSSAPGTIKKTEASQSKDKVPATEDELPAPRL 729
 DB 670 MHMFRSICTIDMPYS-----ENIKGSDLVDFVTAVIKRRDESSSDANPDTHKEN----V 721

QY 730 PDNVRFPVGVDFENPEESCE-----HKTVESIAGPEPLEH-LFHESYHPNTA----- 778
 DB 722 AELEKHAHAIVAELEKHEKHEIAKLGECHKEVLRGLGQHKKEETIILEKHKDVVTKLGE 781

QY 779 ---GNMLR-QDYHTDSEVKIAEQ-----EAKAFVDQLLNGGVLOEFMKQKFKVPSD 825
 DB 782 QHKENIIKLEBEHKDVTGLGDQYKEETAKLKEEHAVVVAELVEEKHKLGECHKEVDELE 841

QY 826 NSFADYVTGOAEVFKAQIALLEQSEDFQFVOANAEVDLEHT-----LG 869
 DB 842 KKHADFVGLGEKHKHAKETAKLEEGH-----KSEMNVEKRRHADFVEGLEEKHKHAKTAKLG 896

QY 870 EAF-----ERFGHVVEESNGSKNPKALKTRQOMVKETGDKTQKTRNHYLLHLEAHN 921

Db 897 EGHREVVAGLEEKHEVVAEL--EEKKEEIAKLEEGHKEVMAELGEKHEVVAAGLEAKH 954
 QY 922 RVOIERRETCPPEL 934
 Db 955 NLEEGHKEMVAEL 967

RESULT 15

T50099
 probable protein-tyrosine phosphatase CDC14 homolog [imported] - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
 C:Accession: T50099
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
 submitted to the EMBL Data Library, February 2000
 A:Reference number: Z25037
 A:Accession: T50099
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-537 <WOO>
 A:Cross-references: EMBL:AL158056; PIDN:CAE76271.1; GSPDB:GN00066; SPDB:SPAC1782.09c
 A:Experimental source: strain 972h(-); cosmid c1782
 C:Genetics:
 A:Gene: SPDB:SPAC1782.09c
 A:Map position: 1
 A:introns: 17/1

Query Match 2.7%; Score 141; DB 2; Length 537;

Best Local Similarity 24.6%; Pred. No. 0.38; Mismatches 85; Indels 82; Gaps 16;
 Matches 70; Conservative 47

QY 37 YNSIVERIRHIFRTAVSSNRCTEYQNIDL-----DCAYITDRIIAIGYPAT 84
 Db 142 YYITIQDCVYGLWRRESS---ILNIRIDVHDYETVERVENGDFNWSPKETAFASP-- 196
 QY 85 GIEANFRNSKVCTQ-----FLTRHKGKGVKVNLRGGYYIDADNFDGNV--- 130
 Db 197 -IQAGWNHASTRPKLPQFAVLVDYFVANK-----VKLIVRLNGPLYDKKTFE-NVGIR 249
 QY 131 ---ICFDMTDHPPSLLEMAPFCREAKWL---EADDKHVIACHKAGKGRGTGMICAL 183
 Db 250 HKEMYFE--DGVPELSLV-----KEFIDLTEEVEDGVIAVCKAGLGTGCLIGAY 300
 QY 184 LIYINFPSPQILDYYSIIRTNNKGVTPSQRYI-----YYHKLREBELNYL 234
 Db 301 LIYKHCFTANEVIAYMRMR---PGMVVGQOHLHINQVHFRAYFYEKAMGRAIQOA 355
 QY 235 PLRMQLIGYVVERPPK-----TWGGGSKIKVEVNGSGTILFKPDP 274
 Db 356 TAAEPL-----ATPPRHPLNATNGTSQ-----SNISTPLPEPTP 389

Search completed: December 10, 2003, 20:35:04
 Job time : 32.8035 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:28:57 ; Search time 16.6821 Seconds
(without alignments)
2711.873 Million cell updates/sec

Title: US-09-205-658A-310
Perfect score: 5168
Sequence: 1 MVTPTDVPDSTRSMARDL.....IAHFSNFSNFDQAIYL 962

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	490.5	9.5	403	1 PTEN HUMAN	O00633 homo sapien
2	490.5	9.5	403	1 PTEN MOUSE	O08586 mus musculu
3	333.5	6.5	551	1 TPTN HUMAN	P56180 homo sapien
4	282	5.5	1744	1 TENS_CHICK	O04205 gallus gall
5	217.5	4.2	910	1 AUXI_BOVIN	Q27974 bos taurus
6	217.5	4.2	1305	1 GAK RAT	P97874 rattus norv
7	209.5	4.1	434	1 YNM8 YEAST	P53916 saccharomyc
8	206	4.0	1311	1 GAK HUMAN	O14976 homo sapien
9	141	2.7	537	1 FLPI SCHPO	Q9p7hl schizosacch
10	138.5	2.7	3259	1 GIAN HUMAN	Q14789 homo sapien
11	136	2.6	1053	1 SPS SOLITU	Q43845 solanum tub
12	134.5	2.6	6632	1 UN89 CAEEL	O01761 caenorhabdi
13	133	2.6	264	1 YLPK CAEEL	P91301 caenorhabdi
14	132.5	2.6	1244	1 YP83 CAEEL	Q09441 caenorhabdi
15	131	2.5	3524	1 ANK2 HUMAN	O01484 homo sapien
16	130.5	2.5	1054	1 SPK1 CRAPL	O04932 cratereostig
17	130.5	2.5	1863	1 BRCl HUMAN	P38398 homo sapien
18	130.5	2.5	1955	1 PUMA PARUN	O61308 parascaris
19	129.5	2.5	786	1 FL10 CHLRE	P45869 chlamydomon
20	129.5	2.5	1226	1 YCS3 YEAST	P25357 saccharomyc
21	128.5	2.5	1195	1 RPOB THEAC	Q03587 thermoplasm
22	127.5	2.5	1142	1 GINA YEAST	Q12263 saccharomyc
23	127	2.5	1453	1 NKCR MOUSE	P30415 mus musculu
24	126.5	2.4	1616	1 P200 MYCCE	Q49429 mycoplasma
25	126.5	2.4	2104	1 MY53 SCHPO	O14157 schizosacch
26	125	2.4	427	1 EB22 YEAST	P36049 saccharomyc
27	125	2.4	5596	1 MDN1 HUMAN	Q9nu22 homo sapien
28	124.5	2.4	1959	1 MYH9 CHICK	P14105 gallus gall
29	124.5	2.4	4344	1 DYHC EMENI	P45444 emericeila
30	124	2.4	1129	1 EG27 CAEEL	Q09228 caenorhabdi
31	124	2.4	1267	1 DHR1 YEAST	Q04217 saccharomyc
32	123.5	2.4	796	1 PRH ARATH	P48785 arabidopsis
33	123.5	2.4	1063	1 CDCE CAEEL	P81299 caenorhabdi

ALIGNMENTS

RESULT 1

ID	PTEN HUMAN	STANDARD;	PRT;	403 AA.
AC	O00633; O02679;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase PTEN (EC 3.1.3.67) (Mutated in multiple advanced cancers 1).			
GN	PTEN OR MMAC1 OR TEP1.			
OS	Homo sapiens (Human), and			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606, 9615;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND VARIANTS.			
RX	SPECIES=Human, and C.familiaris;			
RA	MEDLINE=97245711; PubMed=9090379;			
RA	Steck P.A., Pershouse W.A., Jasser S.A., Lin H., Yung W.K.A.,			
RA	Ligon A.H., Langford L.A., Baumgard M.L., Hattier T., Davis T.,			
RA	Frye C., Hu R., Swedlund B., Teng D.H.F., Tavtigian S.V.;			
RT	"Identification of a candidate tumour suppressor gene, MMAC1, at			
RT	chromosome 10q23.3 that is mutated in multiple advanced cancers.;"			
RL	Nat. Genet. 15:356-363(1997).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RX	SPECIES=Human;			
RA	MEDLINE=97228181; PubMed=9072974;			
RA	Li J., Yen C., Liaw D., Podsypanina K., Bose S., Wang S.I., Puc J.,			
RA	Miliareis C., Rodgers L., McCombie R., Bigner S.H., Giovanella B.C.,			
RA	Ittmann M., Tycko B., Hibshoosh H., Wigler M.H., Parsons R.;			
RT	"PTEN, a putative protein tyrosine phosphatase gene mutated in human			
RT	brain, breast, and prostate cancer.;"			
RL	Science 275:1943-1947(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	SPECIES=Human;			
RA	MEDLINE=97330649; PubMed=9187108;			
RA	Li D.M., Sun H.;			
RT	"TEP1, encoded by a candidate tumor suppressor locus, is a novel			
RT	protein tyrosine phosphatase regulated by transforming growth factor			
RT	beta.;"			
RL	Cancer Res. 57:2124-2129(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	SPECIES=Human;			
RA	Wang S., Li J., Liaw D., Bose S., Podsypanina K., Parsons R.;			
RA	Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	SPECIES=Human;			
RA	Jensen K., de la Bastide M., Parsons R., Parnell L.D., Dedhia N.,			
RA	Gottesman T., Gnoj L., Kaplan N., Lodhi M., Johnson A.F., Shohdy N.,			
RA	Hasegawa A., Haberman K., Huang E.N., Schutz K., Calma C., Granat S.,			
RA	Wigler M., McCombie W.R.;			

34	123	2.4	660	1 SYM BACHD	Q9kgk8 bacillus ha
35	121.5	2.4	1183	1 BMS1 YEAST	Q08965 saccharomyc
36	121.5	2.4	1216	1 PIB1 RAT	P10687 rattus norv
37	121.5	2.4	2869	1 RBP1 PLAVB	Q00798 plasmodium
38	121	2.3	1027	1 EB30 CAEEL	P34441 caenorhabdi
39	120.5	2.3	1208	1 PCP1 SCHPO	Q92351 schizosacch
40	120.5	2.3	1216	1 PIB1 BOVIN	P10894 bos taurus
41	120.5	2.3	1940	1 MYH3 HUMAN	P11055 homo sapien
42	120	2.3	595	1 REB1 KLULA	Q05950 kluyveromyc
43	119.5	2.3	710	1 LT78 ARATH	Q06738 arabidopsis
44	119.5	2.3	1233	1 CIBC BACTM	Q45774 bacillus th
45	119	2.3	770	1 ACE2 YEAST	P21192 saccharomyc

RT "Genomic sequence of PTEN/MMAC1.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RA Gray N.B., Stewart L.M.D., Hamilton J.A., Roberts K.G., Watson G.,
 RA Snary D.;
 RT "Genomic sequence of chromosome 10q23.3 containing exons 6,7,8 and 9
 of the PTEN gene.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RA Tissue=Lung;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gricham J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP CHARACTERIZATION.
 RC SPECIES=Human;
 RX MEDLINE=97404346; PubMed=9256433;
 RA Myers M.P., Stolarov J.P., Eng C., Li J., Wang S.I., Wigler M.H.,
 RA Parsons R., Tonks N.K.;
 RT "P-TEN, the tumor suppressor from human chromosome 10q23, is a dual-
 specificity phosphatase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9052-9057(1997).
 RN [9]
 RP FUNCTION.
 RC SPECIES=Human;
 RX MEDLINE=98256248; PubMed=9593664;
 RA Maehama T., Dixon J.E.;
 RT "The tumor suppressor, PTEN/MMAC1, dephosphorylates the lipid second
 messenger, phosphatidylinositol 3,4,5-trisphosphate.";
 RL J. Biol. Chem. 273:13375-13378(1998).
 RN [10]
 RP PHOSPHORYLATION OF THR-366; SER-370 AND SER-385.
 RC SPECIES=Human;
 RX MEDLINE=2233751; PubMed=12297295;
 RA Miller S., Lou D., Seidman D., Iane W., Neel B.;
 RT "Direct identification of PTEN phosphorylation sites.";
 RL FEBS Lett. 528:145-145(2002).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.10 ANGSTROMS) OF 7-353.
 RC SPECIES=Human;
 RX MEDLINE=20021619; PubMed=1055148;
 RA Lee J.-O., Yang H., Georgescu M.-M., Di Cristofano A., Maehama T.,
 RA Shi Y., Dixon J.E., Pandolfi P., Pavletich N.P.;
 RT "Crystal structure of the PTEN tumor suppressor: implications for its
 phosphoinositide phosphatase activity and membrane association.";
 RL Cell 99:323-334(1999).
 RN [12]
 RP VARIANT CD ASN-137 INS.
 RC SPECIES=Human;
 RX MEDLINE=98007985; PubMed=9345101;
 RA Tsou H.C., Teng D.H.-F., Ping X.L., Brancolini V., Davis T., Hu R.,
 RA Xie X.X., Gruener A.C., Schrager C.A., Christiano A.M., Eng C.,
 RA Steck P., Ott J., Tavtigian S.V., Peacocke M.;
 RT "The role of MMAC1 mutations in early-onset breast cancer: causative
 in association with Cowden syndrome and excluded in BRCA1-negative
 cases.";
 RL Am. J. Hum. Genet. 61:1036-1043(1997).
 RN [13]
 RP VARIANTS CD GLU-343 AND LEU-347.
 RC SPECIES=Human;
 RX MEDLINE=98153621; PubMed=9399897;
 RA Lynch E.D., Ostermeyer E.A., Lee M.K., Arena J.F., Ji H., Dann J.,
 RA Swishel K., Suchard D., MacLeod P.M., Kvinnelsland S., Gjertsen B.T.,
 RA Heimdal K., Lubs H., Moeller P., King M.-C.;
 RT "Inherited mutations in PTEN that are associated with breast cancer,
 Cowden disease, and juvenile polyposis.";
 RL Am. J. Hum. Genet. 61:1254-1260(1997).
 RN [14]
 RP VARIANTS CD ARG-123 AND ARG-124.
 RC SPECIES=Human;
 RX MEDLINE=97402224; PubMed=9259288;
 RA Neelen M.R., van Staveren W.C.G., Peeters E.A.J., Ben Hassel M.,
 RA Gorlin R.J., Hamm H., Lindboe C.F., Fryns J.-P., Sijmons R.H.,
 RA Woods D.G., Mariman E.C.M., Padberg G.W., Kremer H.;
 RT "Germline mutations in the PTEN/MMAC1 gene in patients with Cowden
 disease.";
 RL Hum. Mol. Genet. 6:1383-1397(1997).
 RN [15]
 RP VARIANT CD GLU-129.
 RC SPECIES=Human;
 RX MEDLINE=97285123; PubMed=9140396;
 RA Liaw D., Marsh D.J., Li J., Dahia P.L.M., Wang S.I., Zheng Z.,
 RA Bose S., Call K.M., Tsou H.C., Peacocke M., Eng C., Parsons R.;
 RT "Germline mutations of the PTEN gene in Cowden disease, an inherited
 breast and thyroid cancer syndrome.";
 RL Nat. Genet. 16:64-67(1997).
 RN [16]
 RP VARIANT BZS ARG-170.
 RC SPECIES=Human;
 RX MEDLINE=97382333; PubMed=9241266;
 RA Marsh D.J., Dahia P.L.M., Zheng Z., Liaw D., Parsons R., Gorlin R.J.,
 RA Eng C.;
 RT "Germline mutations in PTEN are present in Bannayan-Zonana syndrome.";
 RL Nat. Genet. 16:333-334(1997).
 RN [17]
 RP VARIANT CD GLU-289.
 RC SPECIES=Human;
 RX MEDLINE=99014194; PubMed=9797362;
 RA Chi S.-G., Kim H.-J., Park B.-J., Min H.-J., Park J.-H., Kim Y.-W.,
 RA Dong S.-H., Kim B.-H., Lee J.-I., Chang Y.-W., Chang R., Kim W.-K.,
 RA Yang M.-H.;
 RT "Mutational abrogation of the PTEN/MMAC1 gene in gastrointestinal
 polyps in patients with Cowden disease.";
 RL Gastroenterology 115:1084-1089(1998).
 RN [18]
 RP VARIANTS CD HIS-68 AND PRO-112.
 RC SPECIES=Human;
 RX MEDLINE=98260873; PubMed=9600246;
 RA Tsou H.C., Ping X.L., Xie X.X., Gruener A.C., Zhang H., Nini R.,
 RA Swishel K., Sybert V., Diamond T.M., Sutphen R., Peacocke M.;
 RT "The genetic basis of Cowden's syndrome: three novel mutations in
 PTEN/MMAC1/TEP1.";
 RL Hum. Genet. 102:467-473(1998).
 RN [19]
 RP VARIANTS CD AND BZS.
 RC SPECIES=Human;
 RX MEDLINE=98133933; PubMed=9467011;
 RA Marsh D.J., Coulon V., Lunetta K.L., Rocca-Serra P., Dahia P.L.M.,
 RA Zheng Z., Liaw D., Caron S., Duboue B., Lin A.Y., Richardson A.-L.,
 RA Bonnetblanc J.-M., Bressieux J.-M., Cabaret-Moreau A., Chompert A.,
 RA Demange L., Eeles R.A., Yehanda A.M., Fearon E.R., Fricker J.-P.,
 RA Gorlin R.J., Hodgson S.V., Huson S., Lacombe D., Leprat F., Odent S.,
 RA Toulouse C., Olopade O.I., Sobol H., Tishler S., Woods C.G.,
 RA Robinson B.G., Weber H.C., Parsons R., Peacocke M., Longy M., Eng C.;

Query Match 9.5%; Score 490.5; DB 1; Length 403;
Best Local Similarity 31.3%; Pred. No. 1.1e-22;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IPTAVSSNRCTEYQNIDLCAYITDRIIAGYPAATGIEANFRNSKVQTOQLTRRHGK 107
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H - K 62

QY 108 G N V K V F N L R G G Y Y D A D N F D G N V I C F D M T D H H P S L E M A P F C R E A K E W L E A D D K H V I A V 167
DB 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P C E D L D Q W L S E D D N H V A I 122

QY 168 H C K A G K R T G V M I C A L L I Y I N F Y P S P R Q I L D Y I S I R T K N K N G V T I P S O R R Y I Y Y H K L R 227
DB 123 H C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y I Y Y S Y L L 182

QY 228 E R E L N Y L P L R M Q L I G V Y V R P P K T W G G S K I K V E G N G S T I L F K P D P L I I S K S N H R E R A 287
DB 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G -----TCNPFQVVCQKVIYSSNSGPTRR- 234

QY 288 T W L N N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I -- R E I G F L K K F S 345
DB 235 -----EDKF-----MYFEFPQPLPVC--GDIKVEFFHKQKMLKK-- 267

QY 346 D O K I G H V W F N T M F -----ACDGLNG-GHFEYVDKTPQVIGDTSIGRKN 389
DB 268 -DKMFHFWNTFFIPGPETSEKVENGLSCQDEIDSICSIERANDNKEYL----- 316

QY 390 G M R R N E T P M R K I D P E T G N E F E S P 412
DB 317 V L T L T K N D L D K A N K D K A N R Y F S P 339

RESULT 2
ID PTEN_MOUSE STANDARD; PRT; 403 AA.

AC O08586;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase PTEN
DE (EC 3.1.3.67) (Mutated in multiple advanced cancers 1).
GN PTEN OR MMAC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97245711; PubMed=9090379;
RA Steck P.A., Pershouse M.A., Jasser S.A., Lin H., Yung W.K.A.,
RA Ligon A.H., Langford L.A., Baumgard M.L., Hattier T., Davis T.,
RA Frye C., Hu R., Swedlund B., Teng D.H.F., Tavtigian S.V.,
RT "Identification of a candidate tumour suppressor gene, MMAC1, at
chromosome 10q23.3 that is mutated in multiple advanced cancers.";
RL Nat. Genet. 15:356-363(1997).
CC 1- FUNCTION: Potential tumor suppressor. Acts as a phosphoinositide
CC 3-phosphatase by regulating PtdIns(3,4,5)P3 levels.
CC 1- CATALYTIC ACTIVITY: Phosphatidylinositol-3,4,5-trisphosphate +
CC H(2)O = phosphatidyl inositol-4,5-bisphosphate + phosphate.
CC 1- COFACTOR: Magnesium.
CC 1- PTM: Phosphorylation results in an inhibited activity towards
CC PIP3 (By similarity).
CC 1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC 1- SIMILARITY: Contains 1 tensin domain.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U92437; AAC53118.1; -.
DR MGI; 109583; Pten.
DR GO; GO:0016506; P:apoptosis activator activity; IMP.
DR GO; GO:0016344; P:phosphatidylinositol-3,4,5-trisphosphate 3-...; IDA.
DR GO; GO:0016477; P:cell migration; IMP.
DR GO; GO:0007417; P:central nervous system development; IMP.
DR GO; GO:0006917; P:induction of apoptosis; IMP.
DR InterPro; IPR000387; TYR phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase; Anti-oncogene; Phosphorylation.
FT DOMAIN 22 303
FT ACT_SITE 124 124
FT MOD_RES 366 366
FT MOD_RES 370 370
FT MOD_RES 385 385
SQ SEQUENCE 403 AA; 47152 MW; 75F97C3DD6843BA9 CRC64;

Query Match 9.5%; Score 490.5; DB 1; Length 403;
Best Local Similarity 31.3%; Pred. No. 1.1e-22;
Matches 120; Conservative 60; Mismatches 138; Indels 65; Gaps 10;

QY 48 IPTAVSSNRCTEYQNIDLCAYITDRIIAGYPAATGIEANFRNSKVQTOQLTRRHGK 107
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I P N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H - K 62

QY 108 G N V K V F N L R G G Y Y D A D N F D G N V I C F D M T D H H P S L E M A P F C R E A K E W L E A D D K H V I A V 167
DB 63 N H Y K I Y N L C A E R H Y D T A K E N C R V A Q Y P F E D H N P P Q L E I K P C E D L D Q W L S E D D N H V A I 122

QY 168 H C K A G K R T G V M I C A L L I Y I N F Y P S P R Q I L D Y I S I R T K N K N G V T I P S O R R Y I Y Y H K L R 227
DB 123 H C K A G K R T G V M I C A Y L L H R G K F L K A Q E A L D F Y G E V R T R D K G V T I P S O R R Y I Y Y S Y L L 182

QY 228 E R E L N Y L P L R M Q L I G V Y V R P P K T W G G S K I K V E G N G S T I L F K P D P L I I S K S N H R E R A 287
DB 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G -----TCNPFQVVCQKVIYSSNSGPTRR- 234

QY 288 T W L N N C D T P N E F D T G E Q K Y H G F V S K R A Y C F M V P E D A P V F E G D V R I D I -- R E I G F L K K F S 345
DB 235 -----EDKF-----MYFEFPQPLPVC--GDIKVEFFHKQKMLKK-- 267

QY 346 D O K I G H V W F N T M F -----ACDGLNG-GHFEYVDKTPQVIGDTSIGRKN 389
DB 268 -DKMFHFWNTFFIPGPETSEKVENGLSCQDEIDSICSIERANDNKEYL----- 316

QY 390 G M R R N E T P M R K I D P E T G N E F E S P 412
DB 317 V L T L T K N D L D K A N K D K A N R Y F S P 339

RESULT 3
ID TPTE_HUMAN STANDARD; PRT; 551 AA.

AC P56180;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Putative protein-tyrosine phosphatase TPTE (EC 3.1.3.48).
GN TPTE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20065863; PubMed=10598804;
RA Chen H., Rossier C., Morris M.A., Scott H.S., Gos A., Bairoch A.,
RA Antonarakis S.E.;

RT "A testis-specific gene, TPTE, encodes a putative transmembrane
 RT tyrosine phosphatase and maps to the pericentromeric region of human
 RT chromosomes 21 and 13, and to chromosomes 15, 22, and Y.";
 RL Hum. Genet. 105:399-409(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20289799; PubMed=10830953;
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
 RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
 RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Reichwald A., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
 RA Rosenthal K., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
 RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordiek G., Hornischer K., Brandt P.,
 RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
 RA Ramer J., Beck A., Klages S., Hennig S., Riessmann L., Dagan E.,
 RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Lehrach H., Reinhardt R., Yaspo M.-L.;
 RT "The DNA sequence of human chromosome 21.";
 RL Nature 405:311-319(2000).
 CC -!- FUNCTION: COULD BE INVOLVED IN SIGNAL TRANSDUCTION.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: EXCLUSIVELY EXPRESSED IN TESTIS.
 CC -!- SIMILARITY: Contains 1 tensin domain.
 CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF007118; AAC34574.1; -;
 DR EMBL; AL163201; CAB90528.1; -;
 DR Genbank; HGNC:12023; TPTE.
 DR MIM; 604336; -;
 DR GO; GO:0016021; C-integral to membrane; TAS.
 DR GO; GO:0006470; P-protein amino acid dephosphorylation; TAS.
 DR GO; GO:0007165; P-signal transduction; TAS.
 DR InterPro; IPR005820; M-channel nlg.
 DR InterPro; IPR000387; Tyr phosphatase.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 KW Hydrolase; Transmembrane.
 FT TRANSMEM 91 111 POTENTIAL.
 FT TRANSMEM 128 148 POTENTIAL.
 FT TRANSMEM 164 184 POTENTIAL.
 FT DOMAIN 236 518 TENSIN.
 FT ACT_SITE 338 338 POTENTIAL.
 FT CONFLICT 386 386 E -> K (IN REF. 2).
 FT CONFLICT 470 470 P -> L (IN REF. 2).
 SQ SEQUENCE 551 AA; 64307 MW; 39C031C7D30685D2 CRC64;
 Query Match 6.5%; Score 333.5; DB 1; Length 551;
 Best Local Similarity 31.5%; Pred. No. 5.8e-13;
 Matches 75; Conservative 51; Mismatches 95; Indels 17; Gaps 4;
 QY 41 IVERINHIF-----RTAVSSNRCRTEYQNIDLCAYITDRIIAGYPATGIEANF 90
 Db 201 ILLRIPLFLHQRKLEKLRVRSNKRRTYRTRDGLDLYTYTERIIAMSPSSGRQSFY 260
 QY 91 RNSKVTQQTFLTRHCKGNKVFNLGGYYVDADNFDGNCVCFDMDTHHPSPLELWAPFC 150
 Db 261 RNPKEVVRFLDKKH-RNHYRVNLCSEAYDPKPHNVRVIMDDHNVPTLHQVVF 319
 QY 151 REAKWELEADKHVIAVHCAGKGRGTGMICALLIIVNFPSPQLLDYYSIIRTKNN-- 208

Db 320 KEVNEWMAQDLENIIVAIHCKGTDRTGTMTWCAFLIASICSTAKESLYYFGERRDKTHS 379
 QY 209 ---KGVITPSORRYIYYHKLRE-RELNYLPLRQOLIGVYVERPKTWGGSKIKVEV 262
 Db 380 EKFGQVETPSQKRYVAYFAQVKHLYNNWLPFRILFIKHFIIYSIPRYVRDLKIQIEM 437
 RESULT 4
 TENS_CHICK
 ID TENS_CHICK STANDARD; PRT; 1744 AA.
 AC Q04205; Q91007; Q92011;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Tensin.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=94350987; PubMed=8071358;
 RA Lo S.H., An Q., Bao S., Wong W.K., Liu Y., Jamney P.A., Hartwig J.H.,
 RA Chen L.B.;
 RT "Molecular cloning of chick cardiac muscle tensin. Full-length cDNA
 RT sequence, expression, and characterization.";
 RL J. Biol. Chem. 269:22310-22319(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=95204530; PubMed=7896874;
 RA Chuang J.Z., Lin D.C., Lin S.;
 RT "Molecular cloning, expression, and mapping of the high affinity
 RT actin-capping domain of chicken cardiac tensin.";
 RL J. Cell Biol. 128:1095-1109(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Chen L.B.;
 RL Submitted (XX-1991) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1469-1744 FROM N.A.
 RC TISSUE=Embryonic chondrocytes, and Embryonic heart;
 RX MEDLINE=94039118; PubMed=8223621;
 RA van de Werken R., Gennari M., Tavella S., Bet P., Molina F.,
 RA Lin S., Cancedda R., Castagnola P.;
 RT "Modulation of tensin and vimentin expression in chick embryo
 RT developing cartilage and cultured differentiating chondrocytes.";
 RL Eur. J. Biochem. 217:781-790(1993).
 RN [5]
 RP SH2 DOMAIN.
 RX MEDLINE=91220073; PubMed=1708917;
 RA Davis S., Lu M.L., Lo S.H., Lin S., Butler J.A., Druker B.J.,
 RA Roberts T.M., An Q., Chen L.B.;
 RT "Presence of an SH2 domain in the actin-binding protein tensin.";
 RL Science 252:712-715(1991).
 CC -!- FUNCTION: MAY BE INVOLVED IN CELL MIGRATION, CARTILAGE DEVELOPMENT
 CC AND IN LINKING SIGNAL TRANSDUCTION PATHWAYS TO THE CYTOSKELETON.
 CC BINDS TO ACTINS AND PHOSPHORYLATED PROTEINS IN SRC-TRANSFORMED
 CC CELLS. MAY BIND ACTIN WITH CAPPING AND BUNDLING PROPERTIES.
 CC -!- SUBCELLULAR LOCATION: LOCALIZES TO ADHERENS JUNCTIONS.
 CC -!- TISSUE SPECIFICITY: HEART, GIZZARD, LUNG AND SKELETAL MUSCLE.
 CC -!- PTM: TYROSINE-PHOSPHORYLATED.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC -----
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DR EMBL; M96625; AAA59053.1; -
DR EMBL; L06652; AAA73949.1; ALT_INIT.
DR EMBL; Z18529; AAA79215.1; ALT_INIT.
DR EMBL; M74165; AAA49087.1; -
DR EMBL; X66286; CAA46992.1; -
DR PIR; A54970; A54970.
DR PIR; S27939; S27939.
DR HSSP; P16277; 1BLK.
DR InterPro; IPR006020; PTB PID.
DR InterPro; IPR000980; SH2.
DR Pfam; PF00017; SH2; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00462; PTB; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
KW Actin-binding; Cytoskeleton; SH2 domain; Phosphorylation.
FT DOMAIN 66 342
FT 1472 1581
FT SH2.
FT C -> R (IN REF. 2).
FT CONFLICT 49 49
FT M -> T (IN REF. 2).
FT CONFLICT 61 61
FT Q -> PR (IN REF. 3).
FT CONFLICT 88 88
FT A -> T (IN REF. 2).
FT CONFLICT 404 404
FT T -> A (IN REF. 2).
FT CONFLICT 452 452
FT DV -> EL (IN REF. 2).
FT CONFLICT 508 509
FT A -> P (IN REF. 2).
FT CONFLICT 522 522
FT R -> A (IN REF. 2).
FT CONFLICT 664 664
FT P -> A (IN REF. 2).
FT CONFLICT 666 666
FT P -> T (IN REF. 2).
FT CONFLICT 875 875
FT P -> A (IN REF. 2).
FT CONFLICT 909 909
FT MISSING (IN REF. 3).
FT CONFLICT 1102 1113
FT G -> A (IN REF. 2).
FT CONFLICT 1240 1240
FT E -> D (IN REF. 2).
FT CONFLICT 1480 1480
FT D -> E (IN REF. 2).
FT CONFLICT 1711 1711
FT SEQUENCE 1744 AA; 187214 MW; 5C3CB86211935524 CRC64;
SQ
Query Match
Best Local Similarity 20.5%; Score 282; DB 1; Length 1744;
Matches 170; Conservative 94; Mismatches 255; Indels 320; Gaps 31;
QY 2 VTTPDPVSTSRWARDLQENPNRQPGPRVSEPHNSIVRIHIFTAIVSSNCRTE 61
DB 29 ITKQVDTED-ATRS-----PRGQAH-----CKASRSMSTAAMESSC--- 65
QY 62 YQNIDLCAIYDRIIAIGYPATGTEANFNKSVQTOQLTRRHGKGNVKNLGGVY 121
DB 66 ----ELDLVIYIERIAVSPSTAEQSPRNLREVAHMLKSKHG-DNVLFLNL-SERRH 119
QY 122 DADNFDGNYICFDMTDHHPSPSELNAPFCREAKEWLEADDKHIVAVHCKAGRGRTGVMTC 181
DB 120 DISKLHPKVLDRGWPLDHTPALEKICSICKAMDTWLNAAAHNVVVLHNGKNGRLGVVA 179
QY 182 ALLIYINFPSPQILDYYSIIRTKNKGVTI--PSQRYIYVYHKLRR--ELNVLPUR 237
DB 180 AYMHYSNIGASADQALDRFAMKRFYEDKVPVQPSQKRIYHFGSLGSGSKMNKPIF 239
QY 238 MQ-----LGVYVERPPKWTGGGSKIKVEVGNGSTILFKPDPL---- 275
DB 240 LHHVIMHGIPNESKGGCPFFLKIYQAMQPVYTSGIYVNGDSQGTICITIEPGLLLKGD 299
QY 276 IISKSNHQERATWLNMCNCTPNEFTDGEQKYGFGVSKRAYCFWVPEDAPVFGVDVIRDI 335
DB 300 ILLKCVHKKFR-----SPTRDVI FRVQFH-----TCVHDLDI-VFGKEDLDEAF 343
QY 336 REIGFLKFKSD-GKHGVWNTWTFACDGLNGHGFYVDKTPYIGDDTSIGKNGMRN 394
DB 344 RD-----ERPFYKGVFEV-----FSY----- 360
QY 395 ETPMRKIDPTEGNEFESPMQVNPGLKXHITEEQAMENYVGMIPPRYTIISKILHEKH 454
DB 361 -----GPEK-----IQGMEHLENGSPSVSDYNTSDPL----- 387
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RESULT 5

AUX1_BOVIN

ID AUX1_BOVIN STANDARD; PRT; 910 AA.

AC Q27974;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Auxilin.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Brain;

RX MEDLINE=95220355; PubMed=7705342;

RA Schroeder S., Morris S.A., Knorr R., Plessmann U., Weber K.,

RA Vinh N.G., Ungewickell E.;

RT "Primary structure of the neuronal clathrin-associated protein

RL auxilin and its expression in bacteria.";

RL Eur. J. Biochem. 228:297-304(1995).

CC -!- FUNCTION: BINDS CLATHRIN HEAVY CHAIN AND PROMOTES ITS ASSEMBLY

CC INTO REGULAR CAGES.

CC -!- TISSUE SPECIFICITY: BRAIN.

CC -!- PTM: THE N-TERMINUS IS BLOCKED.

CC -!- PTM: TARGET FOR COAT-ASSOCIATED CASEIN KINASE II IN VITRO.

CC -!- SIMILARITY: Contains 1 tensin domain.

CC -!- SIMILARITY: Contains 1 J domain.

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CC EMBL; U09237; AAA79037.1; -

DR PIR; S68983; S68983.

DR InterPro; IPR001623; DnaJ_N.

DR InterPro; IPR000387; TYR_phosphatase.

DR Pfam; PF00226; DnaJ; 1.

DR SMART; SM00271; DnaJ; 1.

DR PROSITE; PS00383; TYR_PHOSPHATASE_1; UNKNOWN_1.

DR PROSITE; PS00506; TYR_PHOSPHATASE_2; UNKNOWN_1.

DR PROSITE; PS00636; DNAJ_1; FALSE_NEG.

DR PROSITE; PS0076; DNAJ_2; 1.

KW SH3-binding; Repeat; Phosphorylation.
 FT DOMAIN 33 44 3 X 4 AA APPROXIMATE TANDEM REPEATS.
 FT REPEAT 33 36 1.
 FT REPEAT 37 40 2.
 FT REPEAT 41 44 3.
 FT DOMAIN 60 344 TENSIN.
 FT SITE 406 414 SH3-BINDING (POTENTIAL).
 FT DOMAIN 463 757 PRO-RICH.
 FT DOMAIN 526 529 POLY-GLY.
 FT DOMAIN 846 910 J-DOMAIN.
 SQ SEQUENCE 910 AA; BC156DC1CF3487FD CRC64;
 Query Watch 4.2%; Score 217.5; DB 1; Length 910;
 Best Local Similarity 21.0%; Pred. No. 1.3e-05;
 Matches 211; Conservative 115; Mismatches 371; Indels 307; Gaps 52;
 QY 60 TEYQNDLDCAVITDRIIAIGYPATGIEANFRNSKVQTOQFLTRRHGKGNVNFVNLRGY 119
 DB 54 TSYTKGDLFTVTSRIIVMSPLDSVDIGFRNQVDDIRSLDSRH-LDHYTVYNLSPKS 112
 QY 120 YDAONFDGNVICFMDTHHPSLELMAPFCREAKEWLEADKHVAVHCKAGKGTGMV 179
 DB 113 YRTA-KFHSRVSECSWPIRQAPSLHNLFAVCNMYNLLQNPKNVCVHCLDGRAASSIL 171
 QY 180 ICALLIYINFY--PSRQILDYYSIIRTKNNKVTI-PSORRYIVYHKL---RERELNY 233
 DB 172 VGAMPIFCNLYSTPGAVRLLY-----AKRPGIGLSPSHRRYLGVMCDLLADKPYRPHF 225
 QY 234 LPLRMOLIGVYVERPPKWTGGGSKIKVEVNGSTILFKPDPLIISKNNHQRERATWLNLC 293
 DB 226 KPLTIKSIIV-----SPVPFF---NKQR-----NGC 248
 QY 294 DTNEPDTGEQKH-----GFVSKRAYCFMVPEADPVF-----VEGDVRIDIREI----- 338
 DB 249 RPYCDVLIGETKIYITTCADFERMKEYRV---QDGKIFPLSITVQGDVVVSWYHLRSTIG 305
 QY 339 -GFLKFSOGKICHWFNTMF-----ACDGLNGHGFYVDKTPYICD 381
 DB 306 SRLQAVTNTQIFQGFHGFIPLDITVLKFTKPELDACD-----VPEKYPQLFQ 355
 QY 382 DTSIGRKNRMARNETPMRKIDPETGNEFESPMQ-----IVNPPGLEKHITEQAMENYTN 436
 DB 356 VT-----LDVELQPHDKV-----MELTPPEHYCTKDVPNSILFSSHQEQ--DTLVL 401
 QY 437 YGMIP-----PRY-----TISKIL--HEKHEKGIKVDY-----NDRKLPMGDKSYTES 478
 DB 402 GQAPIDIPDPNPHFGQGGFTSTLCWQDQKSEKFCEDHAALVNQESQSDDELLTSL 461
 QY 479 GKSGDIRGVGGPEIPY-----KAEHVLTFFPVYEMD-----RALKSKDLNNGMKLHV 526
 DB 462 SPHGNANG-----DKPHAARKSKKQEPAPAPPPEDVDLLGLEGSVSKNFSS----- 510
 QY 527 VLRCVDTROSKWMEKSEVFG-----NLAFF-----NEST-RLQALQTM 564
 DB 511 --PAAPPSNELL--SDLFGGGAAGPVQSGQGVDDVDFHPSGPTSTQSTPRSATSTSA 566
 QY 565 NPKWR--PEPCAFSGKAEMHYPPSVRYNSND--GKYNACSNLVSDFFEHNRNIAVLNRY 621
 DB 567 SPTLRVGEATDPFGA-----PS-KPSGQDLGLSPLNTASAS--SDPF----- 607
 QY 622 CRYFYKQSTSRSPRYKRCYCLIKKHFIYIPADTDDVDENGQPFHS--PEHYIKEQEKI 680
 DB 608 ----LQTRSPSPTVHASS-----TPAVNIQPDVSGAWDHTKPGGF----- 645
 QY 681 DAEEAKAGIENTGPGSTSGSS-----APGTIKK-----TEASQSKVKPATEDEL--- 724
 DB 646 ----GWGSKSAATSTGSSHGTPPHONKQPOTLDPADLGTGGSSFASKPTPTCLGG 700
 QY 725 -PPARLPDNRFPVVVG-----VDFENPEEESCEHKVTVESTAGPELHLEHIFHESY 773
 DB 701 FPLSPSPKASQPMGGMGQGGGYNWQOTQSKPQSSMPHSSPQNRPN-----YVNSF 753
 QY 774 HNTAGNMLRDYHTDSEVKIAEQEAKAFVDQLLNGQGVQLQEFMKQPKVPSDNSFADYVT 833

DB 754 SSMPGGQNERGKAAANLEK---QXADAFED-LISQGS-----FNAHKDK----- 794
 QY 834 GOAEVFKAQIALILOSEDFQRVQANAEVDLEHTLGEAFERFGHVHVESNSSKNPKALK 893
 DB 795 -----KGPRTIAE-----MRKEEMAKEMDPEKL-----KILEWIEGKERNIRALL 834
 QY 894 TREQMVKETGKDTQKTRNHVLLHLEAHRVQIERRETCPHELHPE 937
 DB 835 STMHTVLWAGETKWKVPVG--MADLVTPQVQKVKYRKAVLVVHPD 876
 RESULT 6
 GAK_RAT ID GAK_RAT STANDARD; PRT; 1305 AA.
 AC P97874;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cyclin G-associated kinase (EC 2.7.1.-).
 GN GAK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=97165969; PubMed=9013862;
 RA Kanaoka Y., Kimura S.H., Okazaki I., Ikeda M., Nojima H.;
 RT "GAK: a cyclin G associated kinase contains a tensin/auxilin-like domain.";
 RT FEBS Lett. 402:73-80(1997).
 RL
 CC -!- FUNCTION: Associates with cyclin G and CDK5. Seems to act as an auxilin homolog that is involved in the uncoating of clathrin-coated vesicles by Hsc70 in non-neuronal cells. Expression oscillates slightly during the cell cycle, peaking at G1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Localizes to the perinuclear area and to the trans-Golgi network. Also seen on the plasma membrane, probably at focal adhesions (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -!- SIMILARITY: Contains 1 tensin domain.
 CC -!- SIMILARITY: Contains 1 J domain.
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 CC EMBL; D38560; BAA18911.1; -.
 DR PIR; T31096; T31096.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00636; DnaJ_1; FALSE_NEG.
 DR PROSITE; PS00076; DnaJ_2; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Nuclear protein; Endoplasmic reticulum; Cell cycle.
 FT DOMAIN 40 315 PROTEIN KINASE.
 FT ACT SITE 173 173 BY SIMILARITY.
 FT DOMAIN 405 689 TENSIN.
 FT DOMAIN 1241 1305 J-DOMAIN.

SQ SEQUENCE 1305 AA; 143702 MW; 6D36BD38011C44EE CRC64;

Query Match 4.2%; Score 217.5; DB 1; Length 1305;
Best Local Similarity 22.1%; Pred. No. 2.1e-05;
Matches 92; Conservative 56; Mismatches 161; Indels 107; Gaps 17;

QY 62 YQNDLCAYITDRIIAICYPATGTEANFRNSKVOTQOFLTRHKGKGVNKLGGYY 121
DB 401 YAKGLDLSYITSRVAVSFPAEGVESAIKNIEDVRLFLDAKH-PGHVAVNL-SPRIY 458
QY 122 DADNFDGNNVICPDMTDHPPSPLELMAPFCREAKEWLEADDKHVIAVHCKAGKRGTVGMIC 181
DB 459 RASKFHNRVTECGWAVRRAPHLHSLTYLCSRHAWLRDHNRVVCVHCDGGAASAVAVC 518
QY 182 ALLIYINYPSPRLDYYSIIRTKNNKGVITPSORRYIYVHKLRRELNLPLRMQLI 241
DB 519 AFLCFCLFSTAEAAVYFMKRCF-PGIW-PSHKRYIEY-----VC 558
QY 242 GYVVERPPTWGGGSKIVKVEGVNGSTILFKDPDLIISKSNHOR-----ERATWLN 292
DB 559 DMVAEETPHSKMLVK-----SVVNTVPVLFKORNGCRPFCEVYVGEERTV----- 607
QY 293 CDTNPEFDTGEOKYHGFVSKRAYCFWVPEDAPVF-----VEGDVRIDIREI-----GFLK 342
DB 608 -TTSQEDYRME-----FKIEDKAVIDPLGITVQGDVLTILYHARSTLGGRLQ 654
QY 343 -KPSDGKIGHVWNTMF-----ACDGLNGHGFYVDKTOPYIGDDTSI 385
DB 655 AKWAMSKMFQIOFHTGFVRNATTVKFAKYDLDACD-----IQEKYP---DLFQV 701
QY 386 GRKGMRRNETPMRKIDETGNEFSPQIVNPPGLEKHI-----TSEQAMENYTVG 438
DB 702 NLEVEPRDRPSRDV-----PPWENTSRLGNPKILFSNREEQDILSKFG 748

RESULT 7
YNM8 YEAST
ID YNM8 YEAST STANDARD; PRT; 434 AA.
AC PS3916;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical 50.2 kDa protein in CPT1-SPC98 intergenic region.
GN YNL128W OR N1220 OR N1872.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=96109932; PubMed=8619318;
RA Mallet L., Bussereau F., Jacquet M.;
RT "A 43.5 kb segment of yeast chromosome XIV, which contains MPA2,
RT MEP2, CAP/SRV2, NAM9, FRB1/FPRI/RBP1, MOM22 and CPT1, predicts an
RT adenosine deaminase gene and 14 new open reading frames.";
RL Yeast 11:1195-1209(1995).
CC -!- SIMILARITY: SOME, TO PROTEIN-TYROSINE PHOSPHATASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 246843; CAA86897.1; -
DR EMBL; 271404; CAA96010.1; -
DR PIR; S55155; S55155.
DR SGD; S0005072; TRP1.
DR GO; GO:0004437; F:inositol/phosphatidylinositol phosphatase a...; IDA.
DR GO; GO:0007152; P:spore wall assembly (sensu Saccharomycetes); IMP.

DR InterPro; IPR000387; TYR_phosphatase..
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
KW Hypothetical protein; Hydrolase.
SQ SEQUENCE 434 AA; 50152 MW; E56739475D1FA898 CRC64;

Query Match 4.1%; Score 209.5; DB 1; Length 434;
Best Local Similarity 23.8%; Pred. No. 1.4e-05;
Matches 91; Conservative 44; Mismatches 146; Indels 101; Gaps 15;

QY 67 LDCAVITDRIIAIGVPA-TGTEANFRNSKVOTQOFLTRHKGKGVNKLGGYY 121
DB 42 LDISYILVNLVSCYPNTYFKLYRNLSDDLILFLTVYHKGKGNFRIFNFRGEKEDSYK 101
QY 122 DAD-----NFD-----
DB 102 DNDLIGIAAKFESKDFEIQELRSLINDGKIPIIDLETRTLVEETNNVICERIGWLD 161
QY 138 HHPSLELMAPFCREAKEWLEADDKHVIAVHCKAGKRGTVGMICALLI-YNFYSPSPQI 196
DB 162 HFPFPFELLEIVDGIENYLSVSKNRVAVLHCRMGKGRSGMITVAYLMKYLQCPLEGARL 221
QY 197 LDYYSIIRTKNNKGVITPSORRYIYV-----HKLREELNLVPLRMOLIGYVVERPPT 251
DB 222 IFMQARFKYGMNGVTIPSQRYLRYHEFFITHEKAAQE-----GISNE----- 265
QY 252 WGGGSKIKVEGVNGSTILFKDPDLIISKSNHORERATWLNCDTPNEPDTGEOKYHGFVS 311
DB 266 ---AVKFKFKPLAKMTFLRPSSLTISESAVTTKIQHYN--DORNALLTRKVVYSDIMA 320
QY 312 KRA---YCFMVPEADPVFVEGDVRIDIREITGFLKKFSDGKI-----CHVWNTWTFACDG 362
DB 321 HECGNNMTFIFGRDY-LTLENDCRIF-TLGTSKSKAASSIISWTSCASCLNI----- 372
QY 363 GLNGHGFYVDKTOPYIGDDTS 384
DB 373 -----YLETMLHIKDDSS 386

RESULT 8
GAK_HUMAN
ID GAK_HUMAN STANDARD; PRT; 1311 AA.
AC O14976; Q9BVV6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cyclin G-associated kinase (EC 2.7.1.-).
GN GAK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Fibroblast;
RX MEDLINE=97446136; PubMed=9299234;
RA Kimura S.H., Tsuruga H., Yabuta N., Endo Y., Nojima H.;
RT "Structure, expression, and chromosomal localization of human GAK.";
RL Genomics 44:179-187(1997).
RN [2]
RP SEQUENCE OF 981-1311 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,


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CC spindle pole body through to late anaphase.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY, CDC14 SUBFAMILY.
CC -----
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CC -----
CC EMBL; AL158056; CAB76271.1; -
CC PIR; T50099; T50099.
CC HSP; P29350; 1GWZ.
CC GenesDB SPombe; SPAC1782.09c; -
CC InterPro; IPR000340; DS phosphatase.
CC InterPro; IPR000387; TYE phosphatase.
CC Pfam; PF00782; DSPC; 1.
CC PRINTS; PR00700; PRTYPHPTASE.
CC PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
CC PROSITE; PS0056; TYR PHOSPHATASE 2; 1.
CC Hydrolase; Cell cycle; Mitosis; Septation; Nuclear protein;
KW Phosphorylation.
FT ACT SITE 286 286 BY SIMILARITY.
SQ SEQUENCE 537 AA; 60253 MW; F5E50A8C0924C7EA CRC64;

Query Match 2.7%; Score 141; DB 1; Length 537;
Best Local Similarity 24.6%; Pred. No. 0.26; Indels 82; Gaps 16;
Matches 70; Conservative 47; Mismatches 85;

QY 37 YHNSIVIRIRHIFRTAVSSNCRCTEYQNIIDL-----DCAYITRIIAIGYPAT 84
D 142 YVITIDQCVGLWRARESS--ILNIRNIDVDHYETVERVNGDFNWSIPKFIASP-- 196
QY 85 GLEANFRNSKVOTQ-----FLTRHGKGNVKNVFNLRGGYYDANFDQNV--- 130
D 197 -IQAGNWHASTRPKLPQPPFAIVLDFYVANK-----VKLIVRLNGFLYDKKTFE-NVGIR 249
QY 131 ---ICFDMTDHHPPLSLMAPPCREAKWL-----BADDKHVIAVCKAGKGTGMICAL 183
D 250 HKEMVFE--DGVTPSLV-----KEFIDTVEEEDGVIAVCKAGLGTGCLIGAY 300
QY 184 LIYINFPSPROILDYGIIRTKNNKVTIPSQRYI-----YYHKLRLERELNVL 234
D 301 LIYKHF-TANEVIAVMRMR---PGMVVGQQHMLHINQVHFRAFYERKAWGAIQQA 355
QY 235 PLRMOLIGYVERPPK-----TWGGGSKIKVEVNGSTILFKPDP 274
D 356 TAAEPL-----ATPPRHPLNATNGTSQ-----SNISTPLPEPTP 389

RESULT 10
GIAN HUMAN
ID GIAN HUMAN STANDARD; PRT; 3259 AA.
AC Q14789; Q14398;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Golgi autoantigen, golgin subfamily B member 1 (Giantin) (Macrogolgin)
DE (Golgi complex-associated protein, 372-kDa) (GCP372).
GN GOLGB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94187728; PubMed=7511208;
RA Seelig H.P., Schranz P., Schroeter H., Wiemann C., Griffiths G.,
RA Renz M.;
RA "Molecular genetic analyses of a 376-kilodalton Golgi complex membrane
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RT protein (giantin).";
RL Mol. Cell. Biol. 14:2564-2576(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94257116; PubMed=8198703;
RA Seelig H.P., Schranz P., Schroeter H., Wiemann C., Griffiths G.,
RA Renz M.;
RT "Macrogolgin -- a new 376 kD Golgi complex outer membrane protein as
RT target of antibodies in patients with rheumatic diseases and HIV
RT infections.";
RL J. Autoimmun. 7:67-91(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95100974; PubMed=7802676;
RA Sohma M., Misumi Y., Fujiwara T., Nishioka M., Ikehara Y.;
RT "Molecular cloning and sequence analysis of a human 372-kDa protein
RT localized in the Golgi complex.";
RL Biochem. Biophys. Res. Commun. 205:1399-1408(1994).
CC -!- FUNCTION: May participate in forming intercisternal cross-bridges
CC of the Golgi complex.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Membrane-associated protein. Golgi.
CC -!- DISEASE: Antigen in chronic rheumatoid arthritis and in the
CC autoimmune disease Sjogren's syndrome.
CC -----
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CC -----
CC EMBL; X75304; CAA53052.1; -
CC EMBL; D25542; BAA05025.1; -
CC PIR; A56539; A56539.
CC PIR; I52300; I52300.
CC Genes; HGNC:4429; GOLGB1.
CC MIN; 602500; -
CC GO; GO:0000139; C:Golgi membrane; TAS.
CC GO; GO:0005795; C:Golgi stack; TAS.
CC GO; GO:0016021; C:integral to membrane; TAS.
CC GO; GO:0007030; P:Golgi organization and biogenesis; TAS.
KW Golgi stack; Antigen; Coiled coil; Transmembrane.
FT DOMAIN 1 3235
FT TRANSMEM 3236 3256 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 3257 3259 LUMENAL (POTENTIAL).
FT DOMAIN 48 593 COILED COIL (POTENTIAL).
FT DOMAIN 677 1028 COILED COIL (POTENTIAL).
FT DOMAIN 1062 1245 COILED COIL (POTENTIAL).
FT DOMAIN 1301 1779 COILED COIL (POTENTIAL).
FT DOMAIN 1828 3185 COILED COIL (POTENTIAL).
FT DOMAIN 2420 2423 POLY-GLU.
FT DOMAIN 2993 2996 POLY-SER.
FT CONFLICT 1 39 MISSING (IN REF. 3).
FT CONFLICT 215 215 A -> AOLSSM (IN REF. 3).
FT CONFLICT 1765 1765 D -> G (IN REF. 3).
FT CONFLICT 2950 2950 H -> D (IN REF. 3).
SQ SEQUENCE 3259 AA; 376075 MW; 60376A20D8A178DD CRC64;

Query Match 2.7%; Score 138.5; DB 1; Length 3259;
Best Local Similarity 21.7%; Pred. No. 4.6;
Matches 97; Conservative 67; Mismatches 163; Indels 121; Gaps 22;

QY 525 HVVLRCDVTRDSKWKSEKSEVFGNL-----AFINESTRLI-----QALTONPKWRPEPCAFG 576
D 1634 HWV-----EAVRQEKELYKLRSTEANKKETKQLQEAQEEMKMKRKFASKQ 1686
QY 577 SKGAEMHYPPSVRYSSND-----GKYNAGSENLVDSFFEHRLVNLRYCRYK 627
D 1687 QKILELE-----EENDRLAEVHPADGDTAKECNETLS----- 1719
QY 628 QRSTSRSRYPK-KFRYCPLIKKHFYIPADTDDVDENGQFFHSPHVIKEQEKIDAEKAA 686
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DB 1720 SNASKKEELERVMEYETLSKQFSLMSEKDSLSSEVQDLKQKQIEDNVSKQANLEATE-- 1777
QY 687 KGIENTGPSTGS-SAPGTIKKTEASQSDKVPKATEDELPPARLPDNRVFPVGVDPEN 745
DB 1778 KHDNQTNVTEGTQSPGTEBQD-SLSMSTRPTCSSEVPSAKSAN-----PAVSKDFSS 1831
QY 746 PRESECEHTV-----ESIAGFPELHLFHESYH--PNTAGNMLRQDYHTDSVKIAEQEA 799
DB 1832 HDEINNYLQOIDQLKRIAGLEEKQKNEFQSTLENEKNXTLLSQISTKDGELKMLQBEV 1891
QY 800 KAFVDOLLNGQGVLOEFMKQFVPS-----DNSPADVVTGQAEVF 839
DB 1892 TKM--NLIN-QIQBELSRVTKLKTABEEKDDBERLMNQALNGSIGNYC---QDVT 1945
QY 840 KAOI--ALLEQ-----SE-DFORVQANAEVDLEHTLGEAFERFGHVVEESGSK 887
DB 1946 DAQIKNELLESEMKLKKCVSELEEEKQLVKEKTKVESEIRKEY-----LEKIQGAQK 1999
QY 888 NP-----KALKTRQOMVKEGCKD 905
DB 2000 EPGNKSHAKELOELLKQEVKQLQKD 2027
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RESULT 11
SPS_SOLTU STANDARD; PRT; 1053 AA.
AC Q43845;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Phosphate-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-
GN SPS.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_Taxid=4113;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Desiree; TISSUE=Leaf;
RX MEDLINE=95201832; PubMed=7894514;
RA Zremer R., Salanoubat M., Willmitzer L., Sonnewald U.;
RT "Evidence of the crucial role of sucrose synthase for sink strength
RT using transgenic potato plants (Solanum tuberosum L.).";
RL Plant J. 7:97-107(1995).
CC -!- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN
CC THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
CC THEREFORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF
CC PHOTOASSIMILATES OUT OF THE LEAF.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
CC sucrose 6-phosphate.
CC -!- ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND
CC MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
CC -!- PATHWAY: Sucrose synthesis.
CC -!- SUBUNIT: Homodimer or homotetramer (By similarity).
CC -!- PTM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR
CC ENZYME FUNCTION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
CC
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CC EMBL; X73477; CAA51872.1; -.
CC FIR; S34172; S34172.
CC InterPro; IPR001296; Glyco trans 1.
CC Pfam; PF00634; Glycos_transf_1; 1.
```

```
KW Transferase; Glycosyltransferase; Phosphorylation.
SQ SEQUENCE 1053 AA; 118292 MW; D6C933798567B20A CRC64;

Query Match 2.6%; Score 136; DB 1; Length 1053;
Best Local Similarity 18.7%; Pred. No. 1.4;
Matches 154; Conservative 112; Mismatches 283; Indels 276; Gaps 41;

QY 196 ILDYYSIIRTKN---NKGVTIPSQRRYYIYHKLREELNLP--LRMLQIGVVERPPK 250
DB 170 LISUHLIRGENMELGRSDSGTGQVQYVVEL-----ARALGSMGPVYRVDLITRQVSSPEV 225
QY 251 TWGGGSK-----IKVEVGNGS-----TILFKPDPLIISKSNHORERATWLNNDT 295
DB 226 DWSGEPTELAPISTDGLMTGESSGAYIIRIFGP-----REK----- 265
QY 296 PNEFDTGQKHGFVSKRAYCFMVPEDAPVVEGVDRIREIGLFLKFKSGCKTGH--V 352
DB 266 -----YIPKEQLWPYIPE-----FVDGALAHIIQ-----MSKVLGEQIGSGYPV 304
QY 353 W-----FNTMFACDGLN-----GGHPEYVDKTPYIGDDTSIGRKNMRRNET 396
DB 305 WPAIHGHYADGSAALLSGALNVPMFTGHSIGRDKLEQLAQ-----GRSKDEINST 360
QY 397 --PMRKIDPE-----TGNEFESPOQIVN--PPGLEKHITBEQAMENYNTYGM 439
DB 361 YKIMRIEAEELTLDASEIVITSTQEIDEQWLYDGFDPILERKL-RARIKENVSCYGR 419
QY 440 IPPRYTISKILHEKHEKGIKVDYNDKRLPMGDKSYTESGKSGD-----IRGVGGP-- 490
DB 420 FMPRMVAVIPPGMEFHIVPHEGDM-----GETEGSEDGKTDPDPIWAEIMRPFNSPRK 473
QY 491 ---FEIPYKAEHVITPPVYENDRALKSKDLANGMKLHVLRVCVDTTRS----- 536
DB 474 PMILALAPDPDKNLTLLVKAFGECPRLRDAN---LTLMNGNRDNDIMESTNSALLS 530
QY 537 --KMKKESEVEGNLAF--HNES-----TRRLQALTO---MNPKW-RP-----EPCAFG- 576
DB 531 ILKMDIKDLYGVQVAPKHHKQSDVPDIYRLAAKTGVFINPAFIEPGLTLEAAAYGL 590
QY 577 -----SKGAEMHYPPSVRYSSNDGKYNACSENIVSDFFEH-----RNI 615
DB 591 PMVATKNGG---PVDIHRVLDNGLLVDPHQQAIAADALLKLVADKQLWAKCRANGLKNI 646
QY 616 AVLN--RYCRYFYKORSTSRSPRYKPRYCPILKKGFIYPADTDVDSNGQPFHFSPEHY 673
DB 647 HLFWSPEHCKTYLSRIASCKPRQPRWLR-----SIDDDENSET--DSPSDS 691
QY 674 IKE-----QEKIDAEAKAGIENTGPTSGSSAPGTIKKTEA 710
DB 692 LRDIHIDISLNRFSLDGKDNKENADNTLDPEVRRSKLENVLSL---KGALKSTSK 747
QY 711 S-QSDKVKPATEDELPPARLPDNRV---FPVGVGD-----FENPEEESCE 752
DB 748 SWSDDKA-----DQNPAGAKFPARRRRRHIFVIAVDCDASSGLSGSVKKIFEAVEKERAE 802
QY 753 H-----KTVESIAGFEPLHLFHESYHPNTAGNMLRQDYHTDSVKIAEQEAK 800
DB 803 GSIGFILATSNISEVQSFLISEGNMPTDFDAYICNSGDLIYSSFHGEQNPFFVVDLYH 862
QY 801 AFVDOLLNGQGVLOEFMK-----QFKVPSDNSPADY 831
DB 863 SHIEYRWGGEGLRKLTVRWAAASIIDKNGENGHDHIVVEDEDNSADY 907

RESULT 12
UN89 CAEEL
ID UN89 CAEEL STANDARD; PRT; 6632 AA.
AC Q01761; Q17362;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Muscle M-line assembly protein unc-89 (Uncoordinated protein 89).
GN UNC-89 OR C09D1.1.
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FT CONFLICT 2284 2284 E -> G (IN REF. 1).
FT CONFLICT 2297 2297 M -> I (IN REF. 1).
FT CONFLICT 3531 3531 A -> G (IN REF. 1).
FT CONFLICT 3884 3888 DAGEY -> RRRRI (IN REF. 1).
FT CONFLICT 3929 3929 A -> V (IN REF. 1).
FT CONFLICT 5134 5134 A -> P (IN REF. 1).
FT CONFLICT 5145 5145 T -> S (IN REF. 1).
FT CONFLICT 5185 5185 G -> A (IN REF. 1).
FT CONFLICT 5199 5199 K -> N (IN REF. 1).
FT CONFLICT 5202 5202 L -> F (IN REF. 1).
FT CONFLICT 5213 5213 F -> L (IN REF. 1).
FT CONFLICT 6178 6178 A -> G (IN REF. 1).
FT CONFLICT 6268 6268 K -> E (IN REF. 1).
SQ SEQUENCE 6632 AA; 731665 MW; 2623D3EDD62960B89 CRC64;

Query Match 2.6%; Score 134.5; DB 1; Length 6632;
Best Local Similarity 18.9%; Pred. No. 22;
Matches 201; Conservative 134; Mismatches 377; Indels 349; Gaps 53;

QY 45 IRHIFRTAVSSNRCRT-----EYQNDLDCAYITDRIIAG-YPATGI 86
Db 3289 VRELVTVEYKINETATLSVTVKGVDPSPVSEWLVKQGPVQDSSHVIAKVEGSGSYITIK 3348
QY 87 EAFNRSKVQTQOFLTRRHGKGNVKNLGGVYVDADNFD--GNVICFDMTDHPPS-L 143
Db 3349 DARLEDS-----GKYACRATNPAGEAKTEA-NFVVXNLLV-----PPEFV 3387
QY 144 ELMAFPCREAK-----EW-----LEADKRVIAVHCKAG----- 172
Db 3388 EKSLPVLVEKKESTLSVVKVGTPEPSEVDFKDDTPISIDNVHVIOQTAVGFSFSLTIND 3447
QY 173 --KRTGVNIC-----ALLIYNFSPROILDYYSIIRTKNKGVTIPQRYIYY 223
Db 3448 ARQGDVGIVYSCARNEAGEALTANF-----GIIRD-----SIPPE-----FT 3485
QY 224 HKLRE--RELNVLPRLMOLIGVYVERPPKWTGGGSKIKEVGVNGSTILFKPD-PLISK 279
Db 3486 QKLRPLEVREQETLDLKVITGTPV--PNVEW-----FKDDKPINIDN 3526
QY 280 SN-----HQRERATWLNNCDTPEFDTGTEQKYHGVFSKRAYCFMVPE-- 321
Db 3527 SHIFAKDESGHHTLIKQARGEDGVYTCATNE--AGE-----AKTANMAVQERI 3577
QY 322 DAPVFVEG-----DVRIDREIGFLKPSGDKIGHVWNTMFACDG----- 362
Db 3578 EAPLFVQGLKPYEVEQGPDAELVVRVEGKPEPEVKWFKDG-----VPIAIDNQHVIE 3629
QY 363 --GLNGGHPYVDKTPQYIGDDTSGIKNGMRNETPMRKIDPETGNPEPSPQIVNPPG 420
Db 3630 KKGENGSHLVINDT-----NNADFGKYTCQATNKAG-----KDETGVGELKIP----- 3672
QY 421 LEKHTEEQAMENYNYGMIPRYTIS-----KILHEKHEKGIKDDYNDKRLPM 470
Db 3673 --KYSPEKOTAEVVKPLFTEPLEKETFAVEGDTVWLECKVKNESHPO--IKPFKNQOPVEI 3728
QY 471 GKSYTESKSGDIRGVGPPFIPIYKAEHVITFPVYEMDRALKSKDLNMGKMLHVILRC 530
Db 3729 GOHMQLEVLIEDGNIK-----LTIONAKEDVDGAYRCEAVNVAGKA-NTNADLKIQFAAKV 3782
QY 531 VD--TRDSKWE--KSEVFGNLAHNESTR-----LQALTQWNPWK 568
Db 3783 EBHVTDSEQLIEIGQFETVGTASKTDTGRGAEFVELLRSCVTVEKQOAILKCKVKG 3842
QY 569 RPEP-CAFGSKGAEMHYPPSVSYSSNDGKYNKAGCSNLVSDFFEHNRNIAVLNRYCRYFYK 627
Db 3843 EPRPKIKWTKEGKEMSVARVAEHK-----DGLTTLTFDNTVQADAGEY----- 3888
QY 628 QRSTSRSPRFRYCPILIKHFIYPADTDDVDENGQPPFHSPEHYIKEQEKIDAEKAAK 687
Db 3889 -RCEAENEYGSATWEGPII-----VTLEGAP-----KIDGE-APD 3921
QY 688 GIENGTQPS--TSGSSAPGTIKKTEASQSDKVPATE-----DELPPA-----RLPDNVR 734
```

```
Db 3922 FLQPKPAVTVTGETA-----VLEGISGKPKPSVKVKNGEELKPSDRVKIENLDGDTQ 3976
QY 735 RFPVVGVDFENPBESCEHK-----TVESIAGFPLEHLFHESHVHPNTAGNML 782
Db 3977 RLTVTNAKLDMQDEYRCEASNEFGDVMSDVLTVKPEAQVAP-----GFFKELSAIQV 4029
QY 783 RQDYHTDSEVKIA--EQEAKAFVDOL-----LNGOGVLQERMKQKVPSPSDNSFA 829
Db 4030 KETETAKPECKVSGTKPDVKWFKDGTPLUKEDKRVHFESTDDGTOKRLVTEDESKTDDQGNR 4089
QY 830 DYVTGQAAVFKAQIALLEQSEDQFORVQANAEVDEHLEHTLGEAFERFGHVVEESNGSSKNP 889
Db 4090 IEVSNDAVANSKYPLTVVPSETLKIKKGLTDVNV--TQGTKI-----LLSVEVEGPKTV 4143
QY 890 KALKTREOMV-KETGKOTQKTRNNHVLHLLEANHRVQIERRE 929
Db 4144 KWYKGTETVTSQTTKIVQVT-----ESEYKLEIESAE 4176

RESULT 13
YLPK CAEEL
ID YLPK CAEEL STANDARD; PRT; 264 AA.
AC P91301;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 30.3 kDa protein F46F11.3 in chromosome 1.
GN F46F11.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Gattung S.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 tensin domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U88173; AAK21381.1; -.
DR PIR; T25762; T25762.
DR Wormpep; F46F11.3; CE10600.
KW Hypothetical protein.
FT DOMAIN 31 264
SQ SEQUENCE 264 AA; 30300 MW; 3DF3698F292BC5E5 CRC64;

Query Match 2.6%; Score 133; DB 1; Length 264;
Best Local Similarity 21.1%; Pred. No. 0.3;
Matches 40; Conservative 42; Mismatches 90; Indels 18; Gaps 6;

QY 41 IVERIRHIFRTAVSSNRCRTYQNIIDLDCAVITRIIAGYPATGIEANFRSKVQTOF 100
Db 15 LVEKLR-----KQMKDRKEGVQVE--YITSRLIVLSCTSETSERKFVESLLKASQ 65
QY 101 LTRRHGKGNVKNLGGVYVDADNFDGNVTCFDMTDHPPSLELMAPFCEAKEWLEAD 160
Db 66 IQNAHNK-HIRVNVVNSQRRHDISSLD--AIPFGWPESETAPSLKLTCTICKNLDQMLLEH 122
QY 161 DKHVIACHKAGKRTGVMICALLIYNFSPRQILDYYSIIRTKN-----KGVITPSQ 216
Db 123 PLNTAVIFCKGLERCAIVNFMKFNNAISATDSDVDDFRSQWPFSEFLGPDGP--PSY 180
QY 217 RRYIYYHYKL 226
Db 181 KRYLGYFSSL 190
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Db      926 DAGESEKRCVPPSSNPTDYMCDWDCCSYYASPSHVLKHLSEHVAEURLRLCRWGCA 985
QY      933 ELHPEDKIPRIAHFSENSFSDSNFDQA 959
DB      986 DPTFRNRWSLTHIQDHCNEAQLKAA 1012

RESULT 15
ANK2 HUMAN
ID ANK2 HUMAN STANDARD; PRT; 3924 AA.
AC ANK1484;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).
GN ANK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain stem;
RX MEDLINE=91302466; PubMed=1830053;
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
RT "Isolation and characterization of cDNAs encoding human brain
RT ankyrins reveal a family of alternatively spliced genes.";
RN [2]
J. Cell Biol. 114:241-253(1991).
RP REVISIONS.
RA Carpenter S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain stem;
RX MEDLINE=94075409; PubMed=8253844;
RA Chan W., Kordeli E., Bennett V.;
RT "440-kD ankyrinB: structure of the major developmentally regulated
RT domain and selective localization in unmyelinated axons.";
RN [4]
J. Cell Biol. 123:1463-1473(1993).
RP REVISIONS.
RA "Isolation and chromosomal localization of a novel nonerythroid
RL ankyrin gene.";
RX Genomics 10:858-866(1991).
CC -I- FUNCTION: Attach integral membrane proteins to cytoskeletal
CC elements. Also bind to cytoskeletal proteins.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q01484-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q01484-2; Sequence=VSP_000267, VSP_000268;
CC Name=3;
CC IsoId=Q01484-3; Sequence=VSP_000268;
CC -I- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
CC CELLS THROUGHOUT THE BRAIN.
CC -I- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
CC AND FUNCTION (POTENTIAL).
CC -I- SIMILARITY: Contains 23 ANK repeats.
CC -I- SIMILARITY: Contains 1 death domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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Fri Dec 13:18:53 2003

Db 2123 SEETEKAQLHLDQVL 2137

Search completed: December 10, 2003, 20:32:53
Job time : 20.6821 secs

us-09-205 a-310.rsp

Page 15

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:29:32 ; Search time 54.8125 Seconds
(without alignments)
4529.010 Million cell updates/sec

Title: US-09-205-658A-310

Perfect score: 5168

Sequence: 1 MVTPPPDPVSTSRMARDL.....IAHFSNSFSDSNFDQAIYL 962

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mmc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5168	100.0	962	5	O44405 caenorhabdi
2	505.5	9.8	412	13	Q90XY3 fugu rubrip
3	491.5	9.5	403	11	Q54857 rattus norv
4	474.5	9.2	403	4	O43460 homo sapien
5	460.5	8.9	338	4	O14781 homo sapien
6	459.5	8.9	402	13	Q9PUT6 xenopus lae
7	442	8.6	509	5	Q9V3L4 drosophila
8	442	8.6	514	5	Q9V413 drosophila
9	441.5	8.5	506	5	Q9U470 drosophila
10	441.5	8.5	511	5	Q9Y0B5 drosophila
11	438	8.5	632	10	Q8H106 arabidopsis
12	437	8.5	628	10	Q9SN07 arabidopsis
13	435	8.4	418	5	Q9Y0B6 drosophila
14	431	8.3	515	5	Q8T658 dictyosteli
15	431	8.3	533	5	Q8T9S7 dictyosteli
16	403.5	7.8	412	10	Q9FLZ5 arabidopsis

17	401.5	7.8	611	10	Q9LT75 arabidopsis
18	401.5	7.8	611	10	Q8GZT8 arabidopsis
19	400.5	7.7	369	4	Q8IVA5 homo sapien
20	368	7.1	445	4	Q8WML5 homo sapien
21	348.5	6.7	326	4	Q8WML4 homo sapien
22	342	6.6	645	11	Q91X02 mus musculu
23	342	6.6	664	11	Q91X03 mus musculu
24	338.5	6.5	591	11	Q91X01 mus musculu
25	333.5	6.5	533	4	Q8NC58 homo sapien
26	315.5	6.1	1735	4	Q9HBL0 homo sapien
27	301	5.8	1715	6	Q9GLM4 bos taurus
28	273	5.3	222	11	Q8C6V6 mus musculu
29	270	5.2	624	11	Q8BJA7 mus musculu
30	261	5.1	398	4	Q9NV48 homo sapien
31	259.4	5.0	1445	4	Q8IZW7 homo sapien
32	247.5	4.8	348	3	O94526 schizosacch
33	244	4.7	280	11	Q8BSR7 mus musculu
34	240.5	4.7	391	4	Q8NAD0 homo sapien
35	220.5	4.3	913	4	O75061 homo sapien
36	214	4.1	1381	11	Q8CJ95 mus musculu
37	214	4.1	1400	11	Q8CGB6 mus musculu
38	213	4.1	1409	4	Q8NFF9 homo sapien
39	213	4.1	1419	4	Q8NFG0 homo sapien
40	210	4.1	1285	4	Q9UPS7 homo sapien
41	176.5	3.4	885	11	Q8BM74 mus musculu
42	162	3.1	1271	5	Q25860 plasmodium
43	154	3.0	446	5	Q9UAX0 caenorhabdi
44	154	3.0	1233	5	Q8IJ56 plasmodium
45	153.5	3.0	913	4	Q9HCH5 homo sapien

ALIGNMENTS

RESULT 1

O44405 PRELIMINARY; PRT; 962 AA.
 AC O44405; Q9TVU8;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE T07A9.6 protein (DAF-18 protein).
 GN T07A9.6 OR DAF-18.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Scheet P., Maggi L.;
 RT "The sequence of C. elegans cosmid T07A9.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Rouault J.P., Kuwabara P.E., Sinilnikova O., Duret L.,
 RT "Regulation of dauer larva development by the tumor suppressor PTEN
 RT homologue daf-18 in Caenorhabditis elegans.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

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RN RP SEQUENCE FROM N.A.
RX MEDLINE=99102962; PubMed=9885576;
RA Ogg S., Ruvkun G.;
RT "The C. elegans PTEN homolog DAF-18 acts in the insulin receptor-like
RL metabolic signaling pathway.";
RL Mol. Cell 2:887-893(1998).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=99178991; PubMed=10077613;
RA Gil E.B., Malone Link E., Liu L.X., Johnson C.D., Lees J.A.;
RT "Regulation of the insulin-like developmental pathway of
RT Caenorhabditis elegans by a homolog of the PTEN tumor suppressor
RT gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:2925-2930(1999).
DR EMBL; AF036706; AAK39284.1; -.
DR EMBL; AJ131181; CAA10315.1; -.
DR EMBL; AF098286; AAD03420.1; -.
DR EMBL; AF126286; AAD21620.1; -.
DR WormPep; T07A9.6; CE26385.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 962 AA; 110328 MW; 79212EF05C959837 CRC64;

Query Match 100.0%; Score 5168; DB 5; Length 962;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTTPDPVSTSTRSMARDLQENPNRQGEPRVSEPYHNSIVERIRHIFRTAVSSNRCT 60
DB 1 MVTTPDPVSTSTRSMARDLQENPNRQGEPRVSEPYHNSIVERIRHIFRTAVSSNRCT 60

QY 61 EYQNDLDCAYITDRIIAIGYPATGIEANFRNSKVQTFRRHGKGNVFNLRGGY 120
DB 61 EYQNDLDCAYITDRIIAIGYPATGIEANFRNSKVQTFRRHGKGNVFNLRGGY 120

QY 121 YDADNPDGNCVCFDMDTHHPPSLELMAPFCRAKEWLEADDKHVIACHKAGKRTGVM 180
DB 121 YDADNPDGNCVCFDMDTHHPPSLELMAPFCRAKEWLEADDKHVIACHKAGKRTGVM 180

QY 181 CALLIIVINPSPROILDYISIRTKNKGVTIPSORRYIYVYKLRERELNVLPLRMOL 240
DB 181 CALLIIVINPSPROILDYISIRTKNKGVTIPSORRYIYVYKLRERELNVLPLRMOL 240

QY 241 IGVYVERPPTKWTGGGSKIKEVGVNGSTILFKPDPLIISKSNHQRERATWLNKCDTPNEFD 300
DB 241 IGVYVERPPTKWTGGGSKIKEVGVNGSTILFKPDPLIISKSNHQRERATWLNKCDTPNEFD 300

QY 301 TGEQKTHGVSKRAYCFMVPEDAPVPEGVGDVIRIDREIGFLKPKSDGKIGHVWNTMFAC 360
DB 301 TGEQKTHGVSKRAYCFMVPEDAPVPEGVGDVIRIDREIGFLKPKSDGKIGHVWNTMFAC 360

QY 361 DGLNGGHPEYVDKTOPYIGDDTISGRKNGMRNETPMRKIDPETGNEFESPMQIVNPPG 420
DB 361 DGLNGGHPEYVDKTOPYIGDDTISGRKNGMRNETPMRKIDPETGNEFESPMQIVNPPG 420

QY 421 LEKHITEQAMENYNYGMIIPRYTISKILHEKHEKGIIVKDDYNDNRKLPMDGKSYTESGK 480
DB 421 LEKHITEQAMENYNYGMIIPRYTISKILHEKHEKGIIVKDDYNDNRKLPMDGKSYTESGK 480

QY 481 SGDIRGVGPFPIPYKAEHVLTFPVYENDRALKSKDLNNGMKLHVLRVCVTRDSKOME 540
DB 481 SGDIRGVGPFPIPYKAEHVLTFPVYENDRALKSKDLNNGMKLHVLRVCVTRDSKOME 540

QY 541 KSEVFGNLAFHNESTRRLQALQTMNPKWRPECAFGSKGAEMHYPSPVSYSSNDGKYNGA 600
DB 541 KSEVFGNLAFHNESTRRLQALQTMNPKWRPECAFGSKGAEMHYPSPVSYSSNDGKYNGA 600

QY 601 CSENLSVDFEHRNIAVLNRYCRYFYKQSTSRSPRYKFRYCPLIKGHFIYIPADTDDVD 660
DB 601 CSENLSVDFEHRNIAVLNRYCRYFYKQSTSRSPRYKFRYCPLIKGHFIYIPADTDDVD 660

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QY 661 ENGQFFPHSPHYIKEQEKIDAEKAAKGIENTGPSTSGSSAPGTIKKTEASOSDKVKPAT 720
DB 661 ENGQFFPHSPHYIKEQEKIDAEKAAKGIENTGPSTSGSSAPGTIKKTEASOSDKVKPAT 720

QY 721 EDELPPARLPDNNRRFPVGVDFENPEESCEHKTVEISAGPEPLEHLFHESYHNTAGN 780
DB 721 EDELPPARLPDNNRRFPVGVDFENPEESCEHKTVEISAGPEPLEHLFHESYHNTAGN 780

QY 781 MLRDYHTDSEVKIAEQEAKAFVDQLLNGQGVQLQEFMKQFVPSDNSFADYVVGAEVFK 840
DB 781 MLRDYHTDSEVKIAEQEAKAFVDQLLNGQGVQLQEFMKQFVPSDNSFADYVVGAEVFK 840

QY 841 AQIALLEQSEDFQVQANAEVDLEHTLGEAFERFGHVVEESNGSKPKALKKTREOMVK 900
DB 841 AQIALLEQSEDFQVQANAEVDLEHTLGEAFERFGHVVEESNGSKPKALKKTREOMVK 900

QY 901 ETGKDTQKTRNHVLLHLEANHRVQIERRETCPELHPEDKIPRIAHFSENSFSDSNFDOAI 960
DB 901 ETGKDTQKTRNHVLLHLEANHRVQIERRETCPELHPEDKIPRIAHFSENSFSDSNFDOAI 960

QY 961 YL 962
DB 961 YL 962

RESULT 2
Q90XY3
ID Q90XY3 PRELIMINARY; PRT; 412 AA.
AC Q90XY3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE PTEN.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21455682; PubMed=11571655;
RA Yu W.P., Fallen C.J., Tay A., Jirik F.R., Brenner S., Tan Y.H.,
RA Venkatesh B.;
RT "Conserved synteny between the Fugu and human PTEN locus and the
RT evolutionary conservation of vertebrate PTEN function.";
RL Oncogene 20:5554-5561(2001).
DR EMBL; AF325922; AAL08419.1; -.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 412 AA; 47974 MW; 8ABEBD8B71346CE3 CRC64;

Query Match 9.8%; Score 505.5; DB 13; Length 412;
Best Local Similarity 35.7%; Pred. No. 4.1e-27;
Matches 115; Conservative 48; Mismatches 102; Indels 57; Gaps 9;

QY 48 IFRTAVSNCRCTEQYNDLDCAYITDRIIAIGYPATGIEANFRNSKVQTFRRHGK 107
DB 4 IIKWVSNKRYQEDGDFDLTYIPNLIAMGPAERLEGVYRNNDVVRFLDSKH-K 62

QY 108 GNVKFNLRGGYVDADNFDGNVICFDMTHHPPSLELMAPFCRAKEWLEADDKHVIATV 167
DB 63 NHYKIYNLCABRHYDAAKFNCRVAQYPPEDHNPQLEIKPFCELDQWLSDDNHAAI 122

QY 168 HCKAGKGTGVMICALLIIVINPSPROILDYISIRTKNKGVTIPSORRYIYVYKLR 227
DB 123 HCKAGKGTGVMICALLIIVINPSPROILDYISIRTKNKGVTIPSORRYIYVYKLR 182

QY 228 ERELNVLPLRMQLIGVYVVERPPTKWTGGG-----KIKVEGVNGSGTILFKPDPLIIS 278
DB 228 ERELNVLPLRMQLIGVYVVERPPTKWTGGG-----KIKVEGVNGSGTILFKPDPLIIS 278

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Db 183 KNQLEYKPVALLFKHMFETLPMFSGGTGTCNPQVYVQLKVKIHTSNPS----- 230
QY 279 KSNHQRERATWLNCDTNEFDTEGQYKYGVSFKRAYCFMVPEDAPVFEVDGVRIDI--R 336
Db 231 ----HTRR-----EDK-HMF-----FEFPQPLPVC--GDIKVEFFHK 260
QY 337 EIGFLKFKSFGKIGHVWNTMF 358
Db 261 QNKMLKK---DKMFHFWNTFF 279

RESULT 3
O54857
ID O54857 PRELIMINARY; PRT; 403 AA.
AC O54857;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein tyrosine phosphatase and tensin homolog/mutated in multiple
DE advanced cancers protein.
GN PTEN/MMAC1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Roz L., Finocchiaro G.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF017185; AAB96620.1; --
DR InterPro; IPR000397; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00566; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 403 AA; 47118 MW; 243BFE35FE209FE5 CRC64;

Query Match 9.5%; Score 491.5; DB 11; Length 403;
Best Local Similarity 31.3%; Pred. No. 3.8e-26;
Matches 123; Conservative 57; Mismatches 128; Indels 85; Gaps 12;

QY 48 IFRATVSSNRCTEYQNIDLCAYITDRIIAGYATGATGEANFRNSKVQTOQLTRHGK 107
Db 4 I IKEIVSRNKRYQEDGFDLDTYIYVNIAMGFAERLEGVYRNNDVVRFLDSKH-K 62
QY 108 GNVKVFNLRGYYVDADNFDGNCVICFDMTDHPPSLMAPPCEAKEWLEADDKHVIAT 167
Db 63 NHYKYNLCARHYDTAKENCRVAQYPPEDHNPQQLKPKCEDLDQWLSDDNHVAI 122
QY 168 HCKAGKRGTVMICALLIYINFPSPQILDYYSIIRTKNNKGVITPSQRRYIYYHKLR 227
Db 123 HCKAGKRGTVMICALLHRRGKFLKAQALDFYGEVTRDKKGVITPSQRRYIYYSVLL 182
QY 228 BRELVNPLRMQLIGVYVERPPKTWGGG-----KIKVEVNG-GSTILFKPDPLII 277
Db 183 KNHLYRVPVALLFHKKMFETIFMFGSGTCNPQVVCQKLVKIYSSNGPT----- 232
QY 278 KSNHQRERATWLNCDTNEFDTEGQYKYGVSFKRAYCFMVPEDAPVFEVDGVRIDI-- 335
Db 233 ----RRE-----DKLMY-FEFPQPLPVC--GDIKVEFFH 259
QY 336 REIGFLKFKSFGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYI 379
Db 260 QNKMLKK---DKMFHFWNTFFIPGPBETSEKVENGLCQDEISICSIERADNDKEYL 316
QY 380 GDDTSIGRKGRRNETPMRKIDPETGNEFESP 412
Db 317 -----VLTLTKNLDLQKANKRYFSP 339

RESULT 4
O43460
ID O43460 PRELIMINARY; PRT; 403 AA.
AC O43460;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phosphatase and tensin homolog 2 (Fragment).
GN PTH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC MEDLINE=98127441; PubMed=9467947;
RA Kim S.K., Su L.K., Oh Y., Kemp B.L., Hong W.K., Mao L.;
RT "Alterations of PTEN/MMAC1, a candidate tumor suppressor gene, and its
RT homologue, PTH2, in small cell lung cancer cell lines.";
RL Oncogene 16:89-93(1998).
DR EMBL; AF019083; AAC52017.1; --
DR Genew; HGNC:9589; PTENP1.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00566; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
FT NON TER.
SQ SEQUENCE 403 AA; 47163 MW; BDD42A4D0F26B419 CRC64;

Query Match 9.2%; Score 474.5; DB 4; Length 403;
Best Local Similarity 30.1%; Pred. No. 5.9e-25;
Matches 118; Conservative 57; Mismatches 134; Indels 83; Gaps 11;

QY 48 IFRATVSSNRCTEYQNIDLCAYITDRIIAGYATGATGEANFRNSKVQTOQLTRHGK 107
Db 4 I IKEIVSRNKRYQEDGFDLDTYIYVNIAMGFAERLEGVYRNNDVVRFLDSKH-K 62
QY 108 GNVKVFNLRGYYVDADNFDGNCVICFDMTDHPPSLMAPPCEAKEWLEADDKHVIAT 167
Db 63 NHYKYNLCARHYDTAKENCRVAQYPPEDHNPQQLKPKCEDLDQWLSDDNHVAI 122
QY 168 HCKAGKRGTVMICALLIYINFPSPQILDYYSIIRTKNNKGVITPSQRRYIYYHKLR 227
Db 123 HCKAGKRGTVMICALLHRRGKFLKAQALDFYGEVTRDKKGVITPSQRRYIYYSVLL 182
QY 228 BRELVNPLRMQLIGVYVERPPKTWGGG-----KIKVEVNG-GSTILFKPDPLII 278
Db 183 KNHLYRVPVALLFHKKMFETIFMFGSGTCNPQVVCQKLVKIYSSNGP----- 231
QY 279 KSNHQRERATWLNCDTNEFDTEGQYKYGVSFKRAYCFMVPEDAPVFEVDGVRIDI--R 336
Db 232 ----TRW-----EDKF-----MYFEFPQPLPVC--GDIKVEFFHK 260
QY 337 EIGFLKFKSFGKIGHVWNTMF-----ACDGLNG-GHFEYVDKTPQYIG 380
Db 261 QNKMLKK---DKMFHFWNTFFIPGPBETSEKVENGLCQDEISICSIERADNDKEYL- 316
QY 381 DDTSIGRKGRRNETPMRKIDPETGNEFESP 412
Db 317 -----VLTLTKNLDLQKANKRYFSP 339

RESULT 5
O14781
ID O14781 PRELIMINARY; PRT; 338 AA.
AC O14781;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
GN PTEN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
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RP SEQUENCE FROM N.A.
RX MEDLINE=99008335; PubMed=9794233;
RA Forcace E., Biesertveld E.J., Sekido Y., Fong K., Muneer S.,
RA Wistuba I.I., Milchgrub S., Breznicek R., Virmani A., Gazdar A.F.,
RA Minna J.D.;
RT "Mutation analysis of the PTEN/MMAC1 gene in lung cancer.";
RL Oncogene 17:1557-1565(1998).
DR EMBL; AF017999; AAB70558.1; -.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
KW = Hypothetical protein; Hydrolase.
FT NON_TER 1
FT TER 338
SQ SEQUENCE 338 AA; 39899 MW; 63F3F51FBA9FA305 CRC64;
Query Match 8.9%; Score 460.5; DB 4; Length 338;
Best Local Similarity 33.5%; Pred. No. 4.3e-24;
Matches 108; Conservative 47; Mismatches 110; Indels 57; Gaps 8;
QY 48 IFTAVSSNRCTEYQNIIDLCAYITDRIIAGYPATGIEANFRNSKVQTOQLTRRHGK 107
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I Y N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H - K 62
QY 108 G N V K V F N L R G G Y Y D A D N F D G N V I C F D M T D H H P P S L E M A P F C R A K E W L E A D D K H V I A V 167
DB 63 N H Y K I N L C A E R H Y D T A K S N Y R V A Q Y P F E D H N P P Q L E I K P C E D L D Q L S E D D N H V A I 122
QY 168 H C K A G K G R T G V M I C A L L I Y N F P S P R O I L D Y S I I R T K N K G V T I P S R R Y I Y Y H K L R 227
DB 123 H C K A G K G R T G I M I Y A L L H R G K F L K A Q E A L D F Y G E V R T R D K K G V T I P S R R Y I Y Y S Y L V 182
QY 228 E R E L N Y L P L R M Q L I G V Y V R P P K T W G G S - - - - - K I V E G N G S T I L F K P D P L I S 278
DB 183 K N H L D Y R P V A L L F H K M F E T I P M F S G G T C N P Q F V W C L K V M Y S N S G P - - - - - 231
QY 279 K S N H Q R E R A T W L N C D T P N E F D T G E Q Y H G F V S K R A Y C F W P E D A P V F V E G D V R I D I - - R 336
DB 232 - - - - - T R W - - - - - E D K F - - - - - M Y F E P Q L P V C - - G D I K V E F F H K 260
QY 337 E I G F L K K F S D G K I G H W F N T M F 358
DB 261 Q N K M L K K - - - D K M F H W N T F F 279
RESULT 6
Q9PUT6 PRELIMINARY; PRT; 402 AA.
ID Q9PUT6;
AC Q9PUT6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein/lipid phosphatase Pren.
GN Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20021619; PubMed=10555148;
RA Lee J.O., Yang H., Georgescu M.M., Di Cristofano A., Maehama T.,
RA Shi Y., Dixon J.E., Pandolfi P., Pavletich N.P.;
RT "Crystal structure of the PTEN tumor suppressor: implications for its
RT phosphoinositide phosphatase activity and membrane association.";
RL Cell 99:323-334(1999).
DR EMBL; AF144732; RAD46165.1; -.
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase
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SQ SEQUENCE 402 AA; 46878 MW; E61315E2DAB0850F CRC64;
Query Match 8.9%; Score 459.5; DB 13; Length 402;
Best Local Similarity 33.1%; Pred. No. 6.6e-24;
Matches 116; Conservative 59; Mismatches 110; Indels 65; Gaps 12;
QY 48 IFTAVSSNRCTEYQNIIDLCAYITDRIIAGYPATGIEANFRNSKVQTOQLTRRHGK 107
DB 4 I I K E I V S R N K R Y Q E D G F D L D T Y I Y N I I A M G F P A E R L E G Y V R N N I D D V R F L D S K H - K 62
QY 108 G N V K V F N L R G G Y Y D A D N F D G N V I C F D M T D H H P P S L E M A P F C R A K E W L E A D D K H V I A V 167
DB 63 N H Y K I N L C A E R H Y D T A K S N Y R V A Q Y P F E D H N P P Q L E I K P C E D L D Q L S E N E N V A I 121
QY 168 H C K A G K G R T G V M I C A L L I Y N F P S P R O I L D Y S I I R T K N K G V T I P S R R Y I Y Y H K L R 227
DB 122 H C K A G K G R T G V M I C A Y L L H R G K F P R A Q E A L D F Y G E V R T R D K K G V T I P S R R Y I Y Y S Y L L 181
QY 228 E R E L N Y L P L R M Q L I G V Y V R P P K T W G G S K I K V E G N G S T I L F K P D P L I S K S N H Q R E R A 287
DB 182 K N S L E Y R P V P L L F H K I B E T I P - - - - - M F S G S T - - - - - 209
QY 288 T W L N N C D T P N E F D T G E Q Y H G F V S - - - - - K R A - - - - - Y C F M V P E D A P V F V E G D V R I D I - - R E I 338
DB 210 - - - - - C N P - - - - - Q F V V Y Q L K V I F T S T A G P K R A E K L M Y F D F P Q L P V C - - G D I K V E F F H K Q N 260
QY 339 G F L K K F S D G K I G H W F N T M F A C D G L N G C H F E Y V D K T Q P Y I G D D T S I O R K 388
DB 261 K V M K K - - - E K M F H W N T F F I - - - - - P G P E Y S E K V E - - - - - N G T L V G E Q 297
RESULT 7
Q9V3L4 PRELIMINARY; PRT; 509 AA.
ID Q9V3L4;
AC Q9V3L4; Q9U468;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phosphatase and tensin homolog.
GN PTEN OR CG5671.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Florek C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kerchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.
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Db	313	DDV	---HKOSEHKRFSEEFKISIVFEAE-N	FSN	-----DVOAEASEKERNENVLNPE	366
Qy	438	----	GMIPRYTISKILHEKHEGKIVKDDYNDRKLPMDGKSYTESGSGDIRGVCGPPE		492	
Db	361	RSYDLSLSPCYAEKKVL	-----TAIVNDNTT	-----KSQT	-----	391
Qy	493	IPYKAEHHVLTFFPVYVENDRALKSKDLNNGMKLHVLRVCDTRDSKMM	-----EKSEVF	545		
Db	392	--IETLHKDKIVTKIOYDTSNNSKNTSTACKR	-----KOPNSKTLPLSLNDSTKEIK	442		
Qy	546	GNLAFHNESRRLQALQTMNPKWPEPCAFSGKGAEMHYPSVRYSSNDGK	---YNG	--A	600	
Db	443	RNIHFNOPSIKKTDLI	-----KW	-----QNSEVHITSOTR	SINENKNINYSYIT	487
Qy	601	CSEN	604			
Db	488	CKQS	491			
RESULT 8						
ID	Q9V413	PRELIMINARY;	PRT;	514	AA.	
AC	Q9V413;					
DT	01-MAY-2000	(TREMBlrel. 13, Created)				
DT	01-MAY-2000	(TREMBlrel. 13, Last sequence update)				
DT	01-MAR-2003	(TREMBlrel. 23, Last annotation update)				
DE	PTEN	protein.				
OS	PTEN	OR CG5671.				
OS	Drosophila	melanogaster (Fruit fly).				
OC	Eukaryota;	Metazoa;	Arthropoda;	Hexapoda;	Insecta;	
OC	Neoptera;	Endopterygota;	Diptera;	Brachycera;	Muscomorpha;	
OC	Ephydroidea;	Drosophilidae;	Drosophila			
ON	NCBI	TaxID=7227;				
RX	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=BERKELEY;					
RX	MEDLINE=20196006;	PubMed=10731132;				
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A.,	Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A.,	Galle R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M.,	Henderson S.N.,				
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q.,	Chen L.X.,				
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M.,	Pfeiffer B.D.,				
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R.,	Miklos G.L.G.,				
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C.,	Baldwin D.,				
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L.,	Beasley E.M.,				
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D.,	Bolshakov S.,				
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P.,	Brottier P.,				
RA	Burtis K.C., Bueam D.A., Butler H., Cadieu E.,	Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B.,	Davies P.,				
RA	de Pablos B., Delcher A., Deng X., Mays A.D., Dew I.,	Dietz S.M.,				
RA	Donson K., Doup L.E., Downes M., Dugan-Rocha S.,	Dunkov B.C., Dunn P.,				
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S.,	Fleischmann W.,				
RA	Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M.,	Glasser K.,				
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P.,	Harris M.,				
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R.,	Houck J.,				
RA	Hoskin D., Houston K.A., Howland T.J., Wei M.-H.,	Ibegwam C.,				
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,	Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S.,	Kulp D., Lai Z.,				
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z.,	Liang Y., Lin X.,				
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P.,	McPherson D.,				
RA	Merkulov G., Mishina N.V., Mobarry C., Morris J.,	Moshrefi A.,				
RA	Mount S.M., Moy M., Murphy B., Murphy L.,	Muzny D.M., Nelson D.L.,				
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R.,	Pacile J.M.,				
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J.,	Puri V., Reese M.G.,				
RA	Reinert K., Remington K., Saunders R.D.C.,	Scheeler F., Shen H.,				
RA	Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P.,	Smith T.,				
RA	Spier E., Spradling A.C., Stapleton M., Strong R.,	Sun E.,				
RA	Svirskas R., Tector C., Turner R., Venter E.,	Wang A.H., Wang X.,				
RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M.,	Weissenbach J.,				
RA	Williams S.M., Woodage T., Worley K.C., Wu D.,	Yang S., Yao Q.A.,				
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G.,	Zhao Q., Zheng L.,				
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X.,	Zhu S., Zhu X., Smith H.O.,				
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;					

QY 546 GNLAHNESTRRLQALTMQNPWRPEPCAFSGKGAEMHPPSVRYSSNDGKNG--ACSE 603
Db 443 RNHIFNQPSIKKTDLI-----KW-----QNSEVHITRSINENKNI-NYNSYITCKQ 487
QY 604 N 604
Db 488 S 488

RESULT 10
QY0B5 PRELIMINARY; PRT; 511 AA.
AC QY0B5: Q9U469;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE PTEN protein (EC 3.1.3.48) (Phosphatase and tensin homolog).
GN PTEN OR CG5671.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith A.;
RT "Alternative splicing of the Drosophila PTEN Gene."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 100-511 FROM N.A.
RC STRAIN-CANTON-S;
RX MEDLINE=20085000; PubMed=10617573;
RA Gberdhan D.C.I., Paricio N., Goodman E.C., Mlodzik M., Wilson C.;
RT "Drosophila tumor suppressor PTEN controls cell size and number by
antagonising the Chico/Pi3-kinase signaling pathway."
RL Genes Dev. 13:3244-3258(1999).
DR EMBL; AF161258; AAD45363.1; -;
DR EMBL; AF201906; AAF23237.1; -;
DR FlyBase; FBgn0026379; Pten.
DR InterPro; IPR000215; Serpin.
DR InterPro; IPR00387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR PROSITE; PS00383; TYR PHOSPHATASE_1; 1.
DR PROSITE; PS0056; TYR PHOSPHATASE_2; 1.
KW Alternative splicing; Hydrolase.
SQ SEQUENCE 511 AA; 58650 MW; 10AB4A19D3DC04D5 CRC64;

Query Match 8.5%; Score 441.5; DB 5; Length 511;
Best Local Similarity 26.3%; Pred. No. 1.7e-22;
Matches 158; Conservative 82; Mismatches 206; Indels 155; Gaps 27;
QY 42 VERIRHIFRTAVSSNRCTEYQNIDLCAYITDRIAGYPATG-IEANFRNSKVQTOQF 100
Db 5 ISLMNVRNVSKRIYKRGYGLDLDLTINDNIAMGYPADPKLEGIFRNRLDVPKL 64
QY 101 LTRRHGKNVKNLNGVYDADNFDGNVICFDMTDHHPSPLELMAPPCREAKEWLEAD 160
Db 65 LEENHAQ-HYKYNLCERSYDVAKRGKRVAVPPDDHNPPTIELIQPCSDVMWLKED 123
QY 161 DKHIAVHCKAGKGTGMICALLIYINFPSPRQILDYYSITRTNNKNGVTIPSORRYI 220
Db 124 SSVNVAHVCKAGKGTGMICAYLVFSGIKSADEALAWYDEKRTKDRKGVTPSORRYV 183
QY 221 YYHKL-----RRELNYLPLR-----MQLIGYVVERPKTWGGSGKIKVEVNGST 267
Db 184 QYFSLVCSVPYSKSVSLNVCBIRFSESSCVQLGM-VE-----CSISV-LHDSAT 232
QY 268 ILFKPDLILSKSNHQRATWLNCCDTPNEFDTEQKYHGVSKRAVCFWVPEDAPFV 327
Db 233 ENAKPDL-----KTLPIDF-----QKSFVLTIKPSIP--V 261

QY 328 EGDYRIDIREIGFLKKPSDGGKIGHWFWNTMFA-----CDGLNGGHFEYVDKTOPYIG 380
Db 262 SGDVKFEL-----TKKSPDKIICHFWLNTFFVRNYSPECSDGTVN-----KVIHTLSKSEI 312
QY 381 DDTSIGRKNRMNETPMRKIDP--ETGNEFESQWQIVNPPGLEKHITTEOAMENYNY- 437
Db 313 DDV---HKDSEHKRFSSEFKLSIVFEAEV-FSN-----DVQAEASEKERNENLVNFE 360
QY 438 ----GMIPPRYTISKILHEKHEKGIKDDYNDRLKPLMGDKSYTESGSGDVGVPPE 492
Db 361 RSDYSLSPNCYAEKKVL-----TAIVNDNTT-----KSQT----- 391
QY 493 IPIYKAEEHVLTFPVVEMDRALKSKDLNMGKMLHVLRVCDTRDSKWM-----EKSEVF 545
Db 392 --IETLHKDIQVTRIQYDVTSTNSKNTSTACR-----KQPNSTLLPLSLNDSTKEIK 442
QY 546 GNLAHNESTRRLQALTMQNPWRPEPCAFSGKGAEMHPPSVRYSSNDGKNG--ACSE 603
Db 443 RNHIFNQPSIKKTDLI-----KW-----QNSEVHITRSINENKNI-NYNSYITCKQ 487
QY 604 N 604
Db 488 S 488

RESULT 11
QYH106 PRELIMINARY; PRT; 632 AA.
AC QYH106;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative tyrosine phosphatase.
GN AT3G50110.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
RA Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT000931; AAN41331.1; -;
SQ SEQUENCE 632 AA; 70072 MW; B1BDD935DD63083F CRC64;

Query Match 8.5%; Score 438; DB 10; Length 632;
Best Local Similarity 25.5%; Pred. No. 4.1e-22;
Matches 157; Conservative 79; Mismatches 195; Indels 184; Gaps 26;
QY 3 TPDPDVSTSTRSMARDL---QENPNR-----QPGEPVRS 34
Db 91 SPFSIFSSGLSSWAKSKFKQQDPNRTDSCMSAFRTSELGLHLPTKSGEVDGRSS 150
QY 35 -----EPYHNSIVE-----RIRHIFRTAVSSNRCTEYQNIDLCAYITDR 75
Db 151 NTQVGAPESLTKAVDSSRGAVKAMQVKARHI---VSNKRRYQEGEFDLDMTYTEN 206
QY 76 IATGYPATGI-----EAFNFSKVQTOQLTRRHGKNVKNLNGVYDADNFD 127
Db 207 IIAAGFPAGDITSSGLFGFEGLYRNHMEVITKFETHH-KDKYKYNILCERLYDASRFE 265
QY 128 GNVCDFMDTDHHPSPLELMAPPCREAKEWLEADKHVIAVHCKAGKGTGMICALLIYI 187
Db 266 GKVASFPDDHNCPIQLIPSCQSAYTWLKEDIQNVVVHCKAGMARTGLMICLLLYL 325
QY 188 NFYSPRQILDYYSITRTNNKNGVTIPSORRYIYYHYHKLREELNYLP--LRMQLIGV-- 243

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Db 326 KFFPTAEBAIDYNNQKRLDGLKALVLPQIRVYKVERVQNFQDGKVPERRCMLRGLPRL 385
Qy 244 ----YVERPPTKWTGGGSKIKVEGVNGSTILFKPDPDLIISKSHQERATWLNCDTPNEF 299
Db 386 INCPYWRP-----AITISNHTDILF-----STKKHOKTK-----415
Qy 300 DTGEQYKHGFVSKR-AYCFMVPEDAPVF-VEGDVRIDIREIGFLKFKSGKIGHVWNTM 357
Db 416 DLGPEDFWTAKPKGKVVVFAIPEAGLTLAGDFKIHFD-----SDGDF-YCWLNTT 467
Qy 358 FA-----CDG-----GLNGGHFEYV-----DKTQP-----YIGDDTSIGRK 388
Db 468 LTNRTMLKSGDFDGRKRLPAGFHVIEIVMEPDNSQPTKSKSDSTQOQSSSSADS 527
Qy 389 NGMRRNETPMRKIDPETGNEFESPMQIVNPPGLEKHITTEQAMENYTVGMTIPRYTISK 448
Db 528 SKLKNEKDDDDVFSDDGEE-----EGNSQSYSTNEKTASSMHTTSK 569
Qy 449 ILHKEHKEGIVKDDYNDRLKPMGDKSYTESGKSG-----DIRGVGGPFEIPY 495
Db 570 -PHQINEPP-KRDD-----PSANKSVTSSSGHYNIPNNSLAVSDIKAIA-----614
Qy 496 KAEHVLTPPVYEMD 510
Db 615 -ADASVFSFGDEED 628

RESULT 12
Q9SN07 PRELIMINARY; PRT; 628 AA.
AC Q9SN07;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative tyrosine phosphatase.
GN F3A4.190.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucots II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Barges M., Collado M.C., Navarro P., Terol J., Perez-Alonso M.,
RA Newes H.W., Lemcke K., Mayer K.F.X., Queciet F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; ALI32978; CAB62119.1; -
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 628 AA; 69569 MW; DF8AC76D03D7B8CC CRC64;

Query Match 8.5%; Score 437; DB 10; Length 628;
Best Local Similarity 25.5%; Pred. No. 4.8e-22;
Matches 156; Conservative 80; Mismatches 195; Indels 180; Gaps 26;

Qy 3 TTPDPVPTSTSMARDL---QENPNR-----RIRHFTAVSSNCRTEYQNIIDLCAVITDR 34
Db 91 SPFSIFSSGLSSWAKSKFKFQQQDPNRTSGMSAFRTFSELGLHLPTKSGSEVGDSRSS 150
Qy 35 -----EPYHNSIVE-----NRIHFTAVSSNCRTEYQNIIDLCAVITDR 75
Db 151 NTQVGAFPSLTAVVDSRGAVKAMQVKARIH-----VSQNRKRQEGEFDLDMYIYEN 206
Qy 76 IIAIGVPATGI-----EAFNRKSVQTOQFLTRRHGKGNVKNVFNLRGGYGYADNPNF 127
Db 207 IIAAGFPAGDISGLFGFPEGLYRNHMEVIRFFETH-KDKYKVNLCSERLYDASRPE 265
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Qy 128 GNVICFDMTHHPPSLELMAPFCREAKEWLEADKHHVIAVHCAGKAGRTGVMICALLIYI 187
Db 266 GKVASFPDDNCNCPPIQIIPSCASAYTWLKEDIQNVVHCKAGMARTGLMICCLLYL 325
Qy 188 NFYSPRQLDYGIIRTKNNKGVTPISQRRYIYYHKLREELNPLR---MOLIGV- 243
Db 326 KFFPTAEBAIDYNNQKRLDGLKALVLPQIRVYKVERVQNFQDGKVPERRCMLRGLPRL 385
Qy 244 YVERPPTKWTGGGSKIKVEGVNGSTILFKPDPDLIISKSHQERATWLNCDTPNEFDTGE 303
Db 386 YWRP-----AITISNHTDILF-----STKKHOKTK-----DLGP 415
Qy 304 QYKHGFVSKR-AYCFMVPEDAPVF-VEGDVRIDIREIGFLKFKSGKIGHVWNTMFA-- 359
Db 416 EDFWIKAPKGVVFAIPEAGLTLAGDFKIHFD-----SDGDF-YCWLNTTLDN 467
Qy 360 -----CDG-----GLNGGHFEYV-----DKTQP-----YIGDDTSIGRKNGMR 392
Db 468 RTMLKSGDFDGRKRLPAGFHVIEIVMEPDNSQPTKSKSDSTQOQSSSSADS 527
Qy 393 RNETPMRKIDPETGNEFESPMQIVNPPGLEKHITTEQAMENYTVGMTIPRYTISKILHE 452
Db 528 SNEKDDDDVFSDDGEE-----EGNSQSYSTNEKTASSMHTTSK-PHQ 568
Qy 453 KHEGIVKDDYNDRLKPMGDKSYTESGKSG-----DIRGVGGPFEIPYKAE 499
Db 569 INEPP-KRDD-----PSANKSVTSSSGHYNIPNNSLAVSDIKAIA-----ADA 613
Qy 500 HVLTPPVYEMD 510
Db 614 SVFSFGDEED 624

RESULT 13
Q9Y0B6 PRELIMINARY; PRT; 418 AA.
AC Q9Y0B6;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE PTEN1 (EC 3.1.3.48) (CG5671-PC).
GN PTEN OR CG5671.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith A.;
RL "Alternative splicing of the Drosophila PTEN Gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov S.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foaier K., Gabrielian A.E., Garg N.S., Gelbart N.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.
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Db 182 IRESIKYVPRNVTLLKIVLRPLPKEINLSEVDFNSVGNKCVFNSKEHNMVVISKKKT 241
Qy 276 IISK-----SNHQRERATWL-----NN 292
Db 242 VVDKNKDPKKLTKENSEKNIDSSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQ 301
Qy 293 CDPN-----EFD-----TGEQYHGFVSXRAYCFMVPEADAPVFEVDVRI 333
Db 302 VGTVNGNTLHQLGGSQFSLSLDAGNTIGNDEYISF-----EIGALSLAGDIRI 350
Qy 334 DIREIGFLKFGDGKIGHVWNTMFACD-----GGLNGGHFEYVDKTPQYIGDD---T 383
Db 351 E-----FTNK-QDDRMFMFWNTSFVQOLEIIPKSGLDKAH---KDKNHKAFPEDFHVEL 401
Qy 384 SIGRKNMGRRNETPMRKIDPETGNE 408
Db 402 TFDQLDQQQSHTTVVASAEQTNNQ 426

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RESULT 15

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Q8T9S7
ID Q8T9S7 PRELIMINARY; PRT; 533 AA.
AC Q8T9S7;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Pten 3-phosphoinositide phosphatase alpha.
GN PTENA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44889;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ax3;
RA Meili R., Firtel R.A.;
RT "Spatial and temporal regulation of Dictyostelium discoideum chemotaxis by PTEN.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF467431; AAL75566.1; -
DR InterPro; IPR000387; TYR_phosphatase.
DR PROSITE; PS00383; TYR_PHOSPHATASE.1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 533 AA; 59831 MW; 9922F7887D6F9F6A CRC64;

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Query Match 8.3%; Score 431; DB 5; Length 533;
Best Local Similarity 26.3%; Pred. No. 9.9e-22;
Matches 117; Conservative 68; Mismatches 156; Indels 104; Gaps 13;
Qy 47 HIFRTAVSNRCRTEYQNTDLCAYITDRIIAGYDPATGIEANFRNSKVQTOQFLTRRHG 106
Db 3 NLLRVAVSQKRYQNGYDLDLAYITDNIIVAMGFPSEKVEGFRNPMKDVQRFDDQVH- 61
Qy 107 KGNVKNVNLGGVYDADFDGNCVCFDMDTHPPSLMAPPCEAKEWLEADDKHVIA 166
Db 62 KDHFKVNLCSERVYHSKFGYGRVGYPPDFDNNAPQFEMIDAFCDVDWAKEDSKNTAV 121
Qy 167 VHCKAGKGTGMICALLIYINFPSPROILDYISIRTKNNKGVITPSQRYIYYHKL 226
Db 122 IHCKAGKGTGLMICWLMYCGWKNKTEDSLRFAALRTYNQKGVITPSQIRYVGYGFRS 181
Qy 227 RERELNPLRMQLIGVYVERPPKTWG-GGSKIKEVG-----NGSTILFKPDPL 275
Db 182 IRESIKYVPRNVTLLKIVLRPLPKEINLSEVDFNSVGNKCVFNSKEHNMVVISKKKT 241
Qy 276 IISK-----SNHQRERATWL-----NN 292
Db 242 VVDKNKDPKKLTKENSEKNIDSSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQ 301
Qy 293 CDPN-----EFD-----TGEQYHGFVSXRAYCFMVPEADAPVFEVDVRI 333
Db 302 VGTVNGNTLHQLGGSQFSLSLDAGNTIGNDEYISF-----EIGALSLAGDIRI 350

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Qy 334 DIREIGFLKFGDGKIGHVWNTMFACD-----GGLNGGHFEYVDKTPQYIGDD---T 383
Db 351 E-----FTNK-QDDRMFMFWNTSFVQOLEIIPKSGLDKAH---KDKNHKAFPEDFHVEL 401
Qy 384 SIGRKNMGRRNETPMRKIDPETGNE 408
Db 402 TFDQLDQQQSHTTVVASAEQTNNQ 426

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